

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 26, 2003, 12:13:30 ; Search time 33.1474 Seconds
(without alignments)
1045.185 Million cell updates/sec

Title: US-09-989-903-2

Perfect score: 1350

Sequence: 1 KPDMSEMSDPPOPLQOEERYD.....KPRKNVPEVSTLRKLYIQ 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

1: A_Geneseq.101002.*
2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
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23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
24: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1350	100.0	281	20	AAW93592	Mouse caspase-14 p
2	1350	100.0	281	21	AAV93213	Amino acid sequenc
3	1332	98.7	257	21	AAV68864	Amino acid sequenc
4	940.5	69.7	242	21	AAV93214	Amino acid sequenc
5	940.5	69.7	242	23	AAV77980	Full-length human
6	912.5	67.6	242	23	AAV77984	Full-length human
7	892.5	66.1	229	21	AAV68865	Amino acid sequenc
8	804.5	59.6	214	21	AAV93216	Amino acid sequenc
9	692.5	51.3	230	21	AAV93215	Amino acid sequenc
10	427	31.6	234	23	AAU72882	Human aspartyl pro

11	286.5	21.2	261	22	AAE0610	Chimeric cassette
12	276.5	20.5	452	23	ABE10110	Mouse caspase 2 pr
13	276	20.4	277	22	AAU05395	Mouse caspase 3
14	275.5	20.4	435	17	AAE90703	Interleukin-1-beta
15	274.5	20.3	435	16	AAE66771	Human interleukin-
16	274.5	20.3	435	17	AAE98462	Human Ice-ced-3 ho
17	274.5	20.3	435	18	AAE26274	Cell death protein
18	274.5	20.3	435	18	AAE21716	Amino acid sequenc
19	274.5	20.3	435	21	AAE14257	Human Ich-1L prote
20	274.5	20.3	435	22	AAE00599	Human caspase-2, a
21	274.5	20.3	435	23	ABE01217	Human caspase-2, SE
22	274.5	20.3	441	16	AAE66768	Human interleukin-
23	274.5	20.3	441	21	AAE14253	Human Ich-1 protei
24	274	20.3	277	17	AAE00372	Apoptain CYP32beta
25	274	20.3	277	17	AAE00677	Pro-Yama. Homo sa
26	274	20.3	277	17	AAE95831	Human interleukin-
27	274	20.3	277	19	AAE47089	Rat interleukin-1
28	274	20.3	277	19	AAE41688	Amino acid sequenc
29	273	20.2	277	17	AAE16600	Apoptain CYP32a pro
30	273	20.2	277	20	AAE21717	Amino acid sequenc
31	273	20.2	277	22	AAE78712	Pig caspase #2. S
32	273	20.2	277	22	AAU05394	Human caspase 3.
33	273	20.2	277	22	AAE00600	Human caspase-3.
34	273	20.2	277	23	ABU01218	Human caspase-3 SE
35	271	20.1	249	21	AAE26763	Human caspase-1 pr
36	269	19.9	241	22	AAE98654	Caspase-3. Uniden
37	268.5	19.9	245	22	AAE95879	Human caspase-3.
38	265	19.6	503	21	AAE14247	Ced-3 protein. Ca
39	264	19.6	277	19	AAE48945	Mutant human apopa
40	264	19.6	277	19	AAE48937	Mutant human apopa
41	263.5	19.5	497	21	AAE14248	Ced-3 protein. Ca
42	260.5	19.3	435	21	AAE14262	Mutant human Ich-1
43	259	19.2	503	15	AAE47463	Ced-3. Caenorhabd
44	256	19.0	503	15	AAE45289	Ced-3 mutant V280.
45	255.5	18.9	303	18	AAE15247	Cysteine protease

ALIGNMENTS

RESULT 1	
AAW93592	AAW93592 standard; Protein; 281 AA.
ID	
XX	AAW93592;
AC	21-JUN-1999 (first entry)
XX	
XX	Mouse caspase-14 protein.
DE	
XX	
XX	Caspase-14; murine; protease; treatment; apoptotic-related disease;
KW	autoimmune disease; cancer; acquired immunodeficiency syndrome; AIDS;
KW	neurodegenerative disease; ischemic injury; anti-idiotypic antibody;
KW	caspase-14 processing activity; epitope; competitor; modulator.
XX	
OS	Mus gp.
XX	
XX	W09910504-A2.
XX	
XX	04-MAR-1999.
PD	
XX	
PF	26-AUG-1998; 98WO-US17715.
XX	
PR	26-AUG-1997; 97US-0056986.
XX	
XX	(IDUN-) IDUN PHARM INC.
PA	
XX	Alnemri ES, Fernandes-Alnemri T;
PI	WPI: 1999-204670/17.
XX	N-PSDB; AAX23515.
DR	
XX	Newly isolated polynucleotide encoding a caspase-14 polypeptide
PT	

PT useful for identifying (ant)agonists that are useful in the
PT diagnosis and treatment of apoptosis-related diseases

PS Claim 4, Fig 1, 59pp; English.

XX This invention describes a novel murine caspase-14 which has protease
XX activity. The caspase-14 polypeptide is useful for identifying
XX (ant)agonists of the polypeptide, where enzyme activity is measured
XX with a fluorescent substrate (especially DEVD-AMC or YVAD-AMC. Activated
XX caspase-14 is useful for identifying inhibitors or enhancers of
XX caspase-14 activity. The compounds identified by both methods
XX form pharmaceutical compositions for treating apoptotic-related diseases,
XX including autoimmune disease, cancer, acquired immunodeficiency syndrome
XX (AIDS), neurodegenerative diseases and ischemic injury. The
XX anti-caspase-14 antibody is useful for measuring the level of caspase-14
XX in a tissue sample. An antibody that binds to a caspase-14 polypeptide is
XX useful for isolating the polypeptide, and an antibody that binds to the
XX large or small subunit the polypeptide is useful for identifying samples
XX with caspase-14 processing activity. An antibody that binds to caspase-14
XX heterodimer or heterotrimer is useful for isolating caspase-14 with
XX apoptotic activity or in a screening assay to identify (ant)agonists. The
XX antibodies form kits for such purposes. The anti-caspase-14 antibody is
XX also useful for preparing anti-idiotypic antibodies, which mimic a
XX caspase-14 epitope recognized by the anti-caspase-14 antibody. Therefore,
XX the antibody is useful as a competitor of caspase-14 in reducing the
XX level of caspase-14 activity, which reduces the level of apoptotic
XX activity. Oligonucleotides made from the polynucleotides are useful as
XX polymerase chain reaction (PCR) primers or probes to screen genomic or
XX cDNA libraries for similar caspase-14 encoding polynucleotides, or for
XX diagnosis of diseases associated with enhanced or inhibited apoptosis.
XX The isolated caspase-14 gene permits methods of modulating apoptosis
XX for the treatment of human diseases.

XX Sequence 281 AA;

Query Match 100.0%; Score 1350; DB 20; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.5e-130;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPDSEMSDPOLOEERYDMSGARLALTLCVTKARSGSEVDMELERMFRLKESTWK 60
DB 17 KPDSEMSDPOLOEERYDMSGARLALTLCVTKARSGSEVDMELERMFRLKESTWK 76
QY 61 RDPYTAQOFLBEIDFEOQTIDNWEPEVSCAFVYLMHAGEGLLKGEDEKVRLEDLFEVLN 120
DB 77 RDPYTAQOFLBEIDFEOQTIDNWEPEVSCAFVYLMHAGEGLLKGEDEKVRLEDLFEVLN 136
QY 121 NNKCALRGKPKVYIIQACRGEHRDPGEBELRGNEBELGDEBELGDEVAVLKNPPOSIFTY 180
DB 137 NNKCALRGKPKVYIIQACRGEHRDPGEBELRGNEBELGDEBELGDEVAVLKNPPOSIFTY 196
QY 181 TDTLHIYSTVEGYLSYRDEKSGSFIQTLTVDFIHKKGSILELBEITRLMANTVEMOEG 240
DB 197 TDTLHIYSTVEGYLSYRDEKSGSFIQTLTVDFIHKKGSILELBEITRLMANTVEMOEG 256
QY 241 KPRKYNPEVOSTLRKKLYIQ 260
DB 257 KPRKYNPEVOSTLRKKLYIQ 276

RESULT 2
AA93213
ID AA93213 standard; Protein; 281 AA.

XX AAY93213;

XX 04-SEP-2000 (first entry)

XX Amino acid sequence of a murine caspase-14.

XX Caspase-14; cell death specific protease; apoptosis stimulator;
XX apoptosis; AIDS; neurodegenerative disease; ischemic injury.

OS Mus sp.

XX Key Location/Qualifiers
XX Region 1..156
XX Active-site /note="large subunit"
XX Cleavage-site 134..138
XX Cleavage-site 156..157
XX Region 162..163
XX Region 163..257
XX /note="small subunit"

XX MO200028047-A1.

XX 18-MAY-2000.

XX 29-OCT-1999; 99WO-US25523.

XX 06-NOV-1998; 98US-0187789.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES, Fernandez-Alnemri T;

XX WPI; 2000-376558/32.

XX N-PSDB; AAA15163.

XX Novel nucleic acids encoding cell death specific protease termed

XX caspase-14 useful for treating cancers by stimulating apoptosis -

XX Claim 52; Fig 1; 78pp; English.

XX The present sequence represents a murine caspase-14 polypeptide. The
XX polypeptide is a cell death specific protease, and is an apoptosis
XX stimulator. Caspase-14 polynucleotides and polypeptides, and
XX anti-caspase-14 antibodies are useful for treating or reducing the
XX severity of pathological conditions associated with increased or
XX decreased levels of apoptosis. Apoptosis mediated diseases such as
XX AIDS, neurodegenerative diseases and ischemic injury are treated by
XX administering anti-caspase-14 antibodies. The antibody is useful for
XX determining the presence or the level of caspase-14 in tissue sample
XX and also for the isolation of caspase-14 with apoptotic activity or
XX in screening assay to identify an agent that inhibits heterodimer or
XX heterotrimer formation and therefore, apoptosis.

XX Sequence 281 AA;

Query Match 100.0%; Score 1350; DB 21; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.5e-130;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPDSEMSDPOLOEERYDMSGARLALTLCVTKARSGSEVDMELERMFRLKESTWK 60
DB 17 KPDSEMSDPOLOEERYDMSGARLALTLCVTKARSGSEVDMELERMFRLKESTWK 76
QY 61 RDPYTAQOFLBEIDFEOQTIDNWEPEVSCAFVYLMHAGEGLLKGEDEKVRLEDLFEVLN 120
DB 77 RDPYTAQOFLBEIDFEOQTIDNWEPEVSCAFVYLMHAGEGLLKGEDEKVRLEDLFEVLN 136
QY 121 NNKCALRGKPKVYIIQACRGEHRDPGEBELRGNEBELGDEBELGDEVAVLKNPPOSIFTY 180
DB 137 NNKCALRGKPKVYIIQACRGEHRDPGEBELRGNEBELGDEBELGDEVAVLKNPPOSIFTY 196
QY 181 TDTLHIYSTVEGYLSYRDEKSGSFIQTLTVDFIHKKGSILELBEITRLMANTVEMOEG 240
DB 197 TDTLHIYSTVEGYLSYRDEKSGSFIQTLTVDFIHKKGSILELBEITRLMANTVEMOEG 256
QY 241 KPRKYNPEVOSTLRKKLYIQ 260
DB 257 KPRKYNPEVOSTLRKKLYIQ 276

RESULT 3
AAY68864

ID	AAV68864 standard; Protein; 257 AA.
XX	AAV68864;
XX	
XX	16-MAY-2000 (first entry)
XX	
DE	Amino acid sequence of a murine caspase-like polypeptide.
XX	
XX	Mouse; caspase-like polypeptide; human; caspase; apoptosis;
KW	skin disease; keratinisation; wound healing.
XX	
OS	Mus musculus.
XX	
PN	WO200004169-A1.
XX	
PD	27-JAN-2000.
XX	
PF	12-JUL-1999; 99WO-EP04939.
XX	
FR	17-JUL-1998; 98EP-0202422.
XX	
PA	(VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
PI	Van De Creen M, Declercq W, Vandenberghe P, Fiers W;
XX	
XX	WPI; 2000-182433/16.
DR	N-PSDB; AAZ60683.
XX	
PT	New murine and human caspase homologues useful for treating skin
XX	related disorders -
PS	Claim 1; Page 51-52; 68pp; English.
XX	
CC	The present sequence represents a murine caspase-like polypeptide. The
CC	specificity also describes a human caspase-like polypeptide.
CC	Caspases are cysteinyl aspartate-specific proteinases which play a
CC	central role in apoptosis. The polypeptides of the invention are related
CC	to human and murine caspase-2 and human caspase-9, and possess all of
CC	the typical amino acids involved in catalysis, including the QACRG box,
CC	and contain no or only a very short prodomain. mRNA expression of the
CC	homologues of the invention is predominant in the skin. The caspase-like
CC	polypeptides are useful for treating human or animal diseases, such
CC	as skin diseases. They are also useful for screening for compounds that
CC	modulate its activity, i.e. agonists, antagonists, and inhibitors. The
CC	caspase-like polypeptides and polynucleotides are useful for modulating
CC	keratinisation, for diagnosing and treating inappropriate wound
CC	healing.
XX	
XX	
SQ	Sequence 257 AA;
	Query Match 98.7%; Score 1332; DB 21; Length 257;
	Best Local Similarity 100.0%; Pred. No. 1,66-128;
	Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY	4 MESEKSDPQPLGEERYDMSGARLALTLCVTKAREGSEVDMALERMFRYLKESTWKRD 63
DB	1 MESEKSDPQPLGEERYDMSGARLALTLCVTKAREGSEVDMALERMFRYLKESTWKRD 60
QY	64 TAOQLELELDEFOQITDNNMEBPVSCAFVYVLMHAGEEGLKGEDEKKNRLIEDLFEVLANKN 123
DB	61 TAOQLELELDEFOQITDNNMEBPVSCAFVYVLMHAGEEGLKGEDEKKNRLIEDLFEVLANKN 120
QY	124 CALKRGKPKVYIIQACRGHRDPGEELRNGEELGDEELGSEVAVLKNKNPISIPYTD 183
DB	121 CALKRGKPKVYIIQACRGHRDPGEELRNGEELGDEELGSEVAVLKNKNPISIPYTD 180
QY	184 LHIYSTVEGYLSYRDEKSGSFIQTLLTVFIHKKSILELTEEITRLMANTEWQEGKR 243
DB	181 LHIYSTVEGYLSYRDEKSGSFIQTLLTVFIHKKSILELTEEITRLMANTEWQEGKR 240
QY	244 KNPVQSTLRKKLYIQ 260
DB	241 KNPVQSTLRKKLYIQ 257

QY	128	RCKPKVVIIOACRGHRHPGEBELRGNBELGGDEDELGCDE-VAVLKNNDQSIPVTYDTLHI	186
Dd	61	FOEIELEKQQOALIDSSEDDPSCAFVVLMMHGRBGFLKGEGENVKLENLFEDLNKNICAL	120
OY	68	FLEEIDEEQOITDMMEEVSCAFVVLMMHGEGGLIKGDEKKMVRDEDIFEVLYNNKNCAL	127
Dd	1	MSNPRLSEEEKYDKMSGARIALILCYTKAREGESEBDIDLLEHMFOLRPRESTMKRDPTEAQ	60
OY	8	MSDPOILOEERYDKMSGARIALTLCTVKAREGSVEUDMEALEMFRYLKESTMKRDPTAOQ	67
Dd	1	MSNPRLSEEEKYDKMSGARIALILCYTKAREGESEBDIDLLEHMFOLRPRESTMKRDPTEAQ	60
Query Match	69.7%	Score 940.5; DB 21; Length 242;	
Best Local Similarity	71.3%	Pred. No. 2.8e-88;	
Matches	181;	Conservative 31; Mismatches 29; Indels 13; Gaps	2;
Sequence	242 AA;		
XX			
CC		The present sequence represents a human caspase-14 polypeptide. The	
CC		polypeptide is a cell death specific protease, and is an apoptosis	
CC		stimulator. Caspase-14 polynucleotides and polypeptides, and	
CC		anti-caspase-14 antibodies are useful for treating or reducing the	
CC		severity of pathological conditions associated with increased or	
CC		decreased levels of apoptosis. Apoptosis mediated diseases such as	
CC		AIDS, neurodegenerative diseases and ischemic injury are treated by	
CC		administering anti-caspase-14 antibodies. The antibody is useful for	
CC		determining the presence or the level of caspase-14 in tissue sample	
CC		and also for the isolation of caspase-14 with apoptotic activity or	
CC		in screening assay to identify an agent that inhibits heterodimer or	
CC		heterotrimer formation and therefore, apoptosis.	
CC			
PS		Claim 13; Fig 7; 7bpb; English.	
XX			
PI		Alnemri ES, Fernandez-Alnemri T;	
DR		WPI; 2000-376556/32.	
XX		N-PsDB; AAA15164.	
PT		Novel nucleic acids encoding cell death specific protease termed	
PT		caspase-14 useful for treating cancers by stimulating apoptosis -	
XX			
PA		(UYJE-) UNIV JEFFERSON THOMAS.	
XX			
PR		06-NOV-1998; 98US-0187789.	
XX			
PF		29-OCT-1999; 99WO-US25523.	
XX			
PD		18-MAY-2000.	
XX			
PN		WO200028047-A1.	
XX			
FT		Key Location/Qualifiers	
FT		Region 1..146	
FT		/note= "large subunit"	
FT		Active-site 130..134	
FT		Cleavage-site 146..147	
FT		Region 147..242	
FT		/note= "small subunit"	
OS		Homo sapiens.	
XX			
KW		Caspase-14; cell death specific protease; apoptosis stimulator;	
KW		apoptosis; AIDS; neurodegenerative disease; ischemic injury.	
DE		Amino acid sequence of a human caspase-14.	
DT		04-SEP-2000 (first entry)	
AC		AA93214 standard; Protein: 242 AA.	
ID		AA93214	
RESULT 4			

Db	121	RAKPRVYIIQACRGRGRPG-----	ETVGGDEIVMTVKDSPQIIPYTDALHV	168
Qy	187	YSTVEGYLSYHDEKSGSFIOTLDVFIHKKSILEETIRLMANTEVMOEGKPRKVN	246	
Db	169	YSTVEGYIAYRHDDQKSGCFIOTLDVDFPKRGHILLETTRMAEALVQEGKARKTN	228	
Qy	247	PEVOSTLKKRLYLQ	260	
Db	229	PEIQTSLKKRLYLQ	242	

```

RESULT 5
AAG77980
ID      AAG77980 standard; Protein; 242 AA.
XX

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DT	05-APR-2002 (first entry)
XX	
DE	Full-length human caspase-14.
xx	

KW Human; caspase-14; anti-apoptotic; apoptosis.

OS Homo sapiens.

PN WO200181595-A2.

PD 01-NOV-2001.

PF 27-APR-2001; 2001WO-US13831.
yy

PR 27-APR-2000; 2000US-199962P.
YY

PA (KNOL) KNOLL GMBH.
VY

PI Mankovich JA;
VY

DR WPI; 2002-041410/05.
DB N-PSDB: AYK98248

Novel 1501 ated by
XX
DT

PT Novel-isolated human caspase-14 proteins and nucleic acid sequences,
PT useful for identifying modulators of caspase-14 protein that are useful
PT for modulating apoptosis -

PS Claim 20; Fig 1; 58pp; English.

CC The sequence represents the novel full-length human caspase-14 protein,
CC referred to as "caspase-14 NEW" in the specification. The invention
CC relates to a novel isolated human caspase-14 protein comprising an amino
CC acid sequence with WSNPSPLE, at its amino terminus. The caspase-14 of
CC the invention has anti-apoptotic activity. Caspase-14 acts as a modulator
CC of caspase-14 activity. The polypeptide is useful for identifying a
CC compound which is a modulator of human caspase-14 activity, and is also
CC useful for identifying a compound which modulates the interaction of
CC caspase-14 with a target molecule. An antibody to caspase-14 is useful
CC for isolating the protein by standard techniques, and for detecting
CC caspase-14 to evaluate the abundance and expression pattern. The antibody
CC is also useful for diagnostically monitoring protein levels in a tissue
CC as a part of a clinical testing procedure. The polypeptide is useful as a
CC protease to cleave substrates and for inducing apoptosis in cells, in
CC screening assays, and as a bait protein in a two-hybrid or three-hybrid
CC assay to identify other proteins that interact with human caspase-14
CC protein.

SQ Sequence 242 AA;

Query Match	69.7%;	Score 940.5;	DB 23;	Length 242;
Best Local Similarity	71.3%;	Pred. No. 2.8e-88;		
Matches 181;	Conservative 31;	Mismatches 29;	Indels 13;	Gaps 2;

QY 8 MSDDQPLQEEERYDMSGARLALTLCVTKAREGSEVDMEALERFRYLKFESTMKRDPTAOQ 67

Db	1	MSNRSJLEEKYKXDMSGARLAILLVTARSGSSEEDDLALHMFQRLAFSTWKRDPFAEQ	60
Oy	68	FLEELDEFOQITIDMWEPEVSCAFVYVLAHGEGLKEDEKMRLEDFEVLNNKCKAL	12
Db	61	FOEELKEKQOQIDIREDPVSCAFVYVLAHGEGLKEDEMVLENTLFEALNNKCOAL	120
Oy	128	RGRPKVYIIOACRGEHNDPGEELRGNEELGDEELGDE-VAVLKNNPOSIPPTYDTLHI	168
Db	121	RAKPRVYIIOACRGEQNDPG-----EIVSGDEIVMVIKSDPQIIPPTYDNLHV	168
Oy	187	YSTVEGYLSYNHDEKSGSGFIOTLTDVFIHKKGSLLELTTEETRIIMANTEVMOBQSPKXN	246
Db	169	YSTVEGYIAYRHDPKSGSCFIOTLTDVFTFRKGGHILELLETTETRMMAEALVQEGKARKTN	228
Oy	247	PEVOSTLRKKLYLQ 260	
Db	229	PEIOSTLRKKLYLQ 242	

RESULT 6
AAG77984
ID AAG77984 standard; Protein; 242 AA

AC AAG77984;

DT 05-APR-2002 (first entry)

Full-length human caspase-14 old.

KW Human; caspase-14; anti-apoptotic; apoptosis.

OS Homo sapiens.
vxy

PN WO200181595-A2
VY

01-NOV-2001
PD
YY

PF 27-APR-2001; 2001WO-US13831.
YY

PR 27-APR-2000; 2000US-199962P.
YY

PA (KNOL) KNOLL GMBH.
VY

PI Mankovich JA;
XY

PT Novel isolated human caspase-14 proteins and nucleic acid sequences,
PT useful for identifying modulators of caspase-14 protein that are useful
PT for modulating apoptosis -

PS Example; Fig 1; 58pp; English.

CC The sequence represents the full-length human caspase-14 protein,
CC referred to as "Caspase-14 Old" in the specification. The invention
CC relates to a novel isolated human caspase-14 protein comprising an amino
CC acid sequence with MSNPSSLEK, at its amino terminus. The caspase-14 of
CC the invention has anti-apoptotic activity. Caspase-14 acts as a modulator
CC of caspase-14 activity. The polypeptide is useful for identifying a
CC compound which is a modulator of human caspase-14 activity, and is also
CC useful for identifying a compound which modulates the interaction of
CC caspase-14 with a target molecule. An antibody to caspase-14 is useful
CC for isolating the protein by standard techniques, and for detecting
CC caspase-14 to evaluate the abundance and expression pattern. The antibody
CC is also useful for diagnostically monitoring protein levels in a tissue
CC as a part of a clinical testing procedure. The polypeptide is useful as a
CC protease to cleave substrates and for inducing apoptosis in cells, in
CC screening assays, and as a bait protein in a two-hybrid or three-hybrid
CC assay to identify other proteins that interact with human caspase-14
CC protein.

SQ Sequence 242 AA;

[illegible]

RESULT 7
AA168865
ID AA168865 standard; Protein; 229 AA.
AC
XX AAY68865;
XX
DT 16-MAY-2000 (first entry)
XX
DE Amino acid sequence of a human caspase-1-like polypeptide.
XX
XX
XX Mouse; caspase-1-like polypeptide; human; caspase; apoptosis;
KM skin disease; keratinisation; wound healing.
XX
XX Homo sapiens.
OS
PN MO200004169-A1.
PN
PD 27-JAN-2000.
XX
XX
PF 12-JUL-1999; 99MO-EP04939.
XX
XX 17-JUL-1998; 98EP-0202422.
XX
XX (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
PA
PI Van De Craen M, Declercq W, Vandenabeele P, Fiers W;
XX
XX WPI; 2000-182433/16.
DR
DR N-PSDB; AA260684.
XX
XX
PT New murine and human caspase homologues useful for treating skin
PT related disorders -
PS
PS Claim 2; Page 53-54; 68pp; English.
XX
XX
XX The present sequence represents a human caspase-1-like polypeptide.
CC The specification also describes a murine caspase-1-like polypeptide.
CC Caspases are cysteine1 aspartate-specific proteinases which play a
CC central role in apoptosis. The polypeptides of the invention are related
CC to human and murine caspase-2 and human caspase-9, and possess all of
CC the typical amino acids involved in catalysis, including the QACRG box,
CC and contain no or only a very short prodomain. mRNA expression of the
CC homologues of the invention is predominant in the skin. The caspase-1-like
CC polypeptides are useful for treating human or animal diseases, such
CC as skin diseases. They are also useful for screening for compounds that
CC modulate its activity, i.e. agonists, antagonists, and inhibitors. The
CC caspase-1-like polypeptides and polynucleotides are useful for modulating
CC keratinisation, for diagnosing and treating inappropriate wound

CC	healing.	
XX		
SQ	Sequence	229 AA;

	Score	DB 21	Length	229
Query Match	65.1%			
Best Local Similarity	71.8%			
Matches 173; Conservative	27			
			Indels	13
			Gaps	2

QY	21	MSGAPLALTLCTVKARBES	EVDMALEMRPFYLF	FESTMKRDP	PAQPL	LELDE	FQOTID	80
		1	MSGAPLALTLCTVKARBES	EEDLDAL	HEMFQ	LF	ESTMKRDP	PAEQF
Db								60
QY	81	NWEBSVSCAFVULMAHGE	ELGLKGEDEKMY	LEDLF	VELNNKNC	KALARG	PKVYII	IOACR
		:	:	:	:	:	:	:
Db	61	SREDPVS	CAFVULMAHGE	ELGLKGEDE	KMYLENL	FEALNNKNC	QALARP	KVYII
								IOACR
QY	141	GEHRDPGE	ELGNELGDE	DELGEDE	-VANL	KNNP	OSIPY	DTLHLY
		:	:	:	:	:	:	:
Db	121	GEORBP	PG-----	ELVGGDE	BEI	WVMI	KOSP	PIPY
								TALH
QY	200	EKSGSG	FIOTLTDV	FLHKKGS	ILTEEL	TEITRL	MANT	EVMOEG
		:	:	:	:	:	:	:
Db	169	QKSGSG	FIOTLTDV	FLTKRKH	ILTEEL	TEVTRM	MAEL	VQEG
								KARK
QY	260	Q	260					
Db	229	Q	229					

RESULT 8
AAV93216
ID AAV93216 standard; Protein; 214 AA

AC AAY93216;

DT 04-SEP-2000 (first entry)

DE Amino acid sequence of a human caspase-14 splice variant.

KW Caspase-14; cell death specific protease; apoptosis stimulator; apoptosis; AIDS; neurodegenerative disease; ischemic injury.

OS Homo sapiens.

...	Key	Location/Qualifiers
FH		

XX

XX

XX

XX

XX

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466
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XX XX

DR N-PSDB; AAA15166.

PT Novel nucleic acids

XX XX

XX

CC polypeptide is a cell death specific protease, and is an apoptosis

CC anti-caspase-14 antibodies are useful for treating or reducing the

CC decreased levels of apoptosis. Apoptosis mediated diseases such as

CC AIDS, neurodegenerative diseases and ischemic injury are treated by
 CC administering anti-caspase-14 antibodies. The antibody is useful for
 CC determining the presence or the level of caspase-14 in tissue sample
 CC and also for the isolation of caspase-14 with apoptotic activity or
 CC in screening assay to identify an agent that inhibits heterodimer or
 CC heterotrimer formation and therefore, apoptosis.

XX Sequence 214 AA;

Query Match 59.6%; Score 804.5; DB 21; Length 214;
 Best Local Similarity 63.0%; Pred. No. 2.3e-74;
 Matches 160; Conservative 27; Mismatches 26; Indels 41; Gaps 3;

QY 8 MSDDPQLOEERYDMSGARLALTLCTVKAREGSEVDMALEHMFYKPESTMKSDPTAAQ 67
 Db 1 MSNRSLEEEKYDMSGARLALTLCTVKAREGSE----- 34
 QY 68 FLEELDFQOTIDNWEBPVSCAFVVLMAHGBEGLKGEDEKVRLEDLFEVLNNKNCAL 127
 Db 35 --EELEKFOQAIDSRDEDPVSCAFVVLMAHGBEGLKGEDEKVRLEDLFEVLNNKNCAL 92
 QY 128 RGRKRVYIIQACRGEHRDPGEBELRGNEELGDEELGDE--VAVLKNNPQSIPTYDTLHI 186
 Db 93 RAKPRVYIIQACRGEHRDPG-----ETVGDEIYMWIKDSPQITPTDYLHV 140
 QY 187 YSTVEGYLSYHNDKSGSFIOTLDVFIHKGSILELTEITRLMANTENVQEGKPRKN 246
 Db 141 YSTVEGYIAYHNDKSGSFIOTLDVFIHKGHILELLETVRRMAELVQEGKARKTN 200
 QY 247 PEVOSTLRKRLYLQ 260
 Db 201 PEIOTLRKRLYLQ 214

RESULT 9
 AAY93215

ID AAY93215 standard; Protein; 230 AA.

XX AC AAY93215;

XX DT 04-SEP-2000 (first entry)

XX DE Amino acid sequence of a human caspase-14 splice variant.

XX KW Caspase-14; cell death specific protease; apoptosis stimulator;
 KW apoptosis; AIDS; neurodegenerative disease; ischemic injury.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Active-site 130..134

XX PN WO200028047-A1.

XX PD 18-MAY-2000.

XX PF 29-OCT-1999; 99WO-US25523.

XX PR 06-NOV-1998; 98US-0187789.

XX PA (UYJE-) UNIV JEFFERSON THOMAS.

XX PI Alnemri ES, Fernandez-Alnemri T;

XX DR WPI; 2000-376558/32.

XX DR N-PSDB; AAA15165.

XX PT Novel nucleic acids encoding cell death specific protease termed

XX PS caspase-14 useful for treating cancers by stimulating apoptosis

XX CC Claim 41; Fig 8; 78pp; English.

XX CC The present sequence represents a human caspase-14 splice variant. The

CC polypeptide is a cell death specific protease, and is an apoptosis
 CC stimulator. Caspase-14 polynucleotides and polypeptides, and
 CC anti-caspase-14 antibodies are useful for treating or reducing the
 CC severity of pathological conditions associated with increased or
 CC decreased levels of apoptosis. Apoptosis mediated diseases such as
 CC AIDS, neurodegenerative diseases and ischemic injury are treated by
 CC administering anti-caspase-14 antibodies. The antibody is useful for
 CC determining the presence or the level of caspase-14 in tissue sample
 CC and also for the isolation of caspase-14 with apoptotic activity or
 CC in screening assay to identify an agent that inhibits heterodimer or
 CC heterotrimer formation and therefore, apoptosis.

XX Sequence 230 AA;

Query Match 51.3%; Score 692.5; DB 21; Length 230;
 Best Local Similarity 72.0%; Pred. No. 8.7e-63;
 Matches 134; Conservative 22; Mismatches 17; Indels 13; Gaps 2;

QY 8 MSDDPQLOEERYDMSGARLALTLCTVKAREGSEVDMALEHMFYKPESTMKSDPTAAQ 67
 Db 1 MSNRSLEEEKYDMSGARLALTLCTVKAREGSEBDLALHMFQRLFEETMKSDPTAAQ 60
 QY 68 FLEELDFQOTIDNWEBPVSCAFVVLMAHGBEGLKGEDEKVRLEDLFEVLNNKNCAL 127
 Db 61 FOEELKFOQAIDSRDEDPVSCAFVVLMAHGBEGLKGEDEKVRLEDLFEVLNNKNCAL 120
 QY 128 RGRKRVYIIQACRGEHRDPGEBELRGNEELGDEELGDE--VAVLKNNPQSIPTYDTLHI 186
 Db 121 RAKPRVYIIQACRGEHRDPG-----ETVGDEIYMWIKDSPQITPTDYLHV 168
 QY 187 YSTVEG 192
 Db 169 YSTVEG 174

RESULT 10
 AAU72882

ID AAU72882 standard; Protein; 234 AA.

XX AC AAU72882;

XX DT 26-FEB-2002 (first entry)

XX DE Human aspartyl protease partial protein sequence #7.

XX KW Human; protease; PCR primer; cytosolic; immunomodulator; cardiant;
 KW vasotropic; antimigraine; analgesic; endocrine; nootropic; tranquiliser;
 KW hypertensive; hypotensive; neuroleptic; neuroprotective; anabolic;
 KW anorectic; antiinflammatory; aspartyl protease; cysteine protease;
 KW metalloprotease; serine protease; cancer; haematopoietic; breast; colon;
 KW lung; prostate; cervical; brain; ovarian; bladder; kidney; pain;
 KW immune-related disease; cardiovascular disease; neuronal disease;
 KW migraine; sexual dysfunction; mood disorder; attention disorder;
 KW cognition disorder; hypotension; hypertension; psychotic disorder;
 KW dyskinesia; metabolic disorder; inflammatory disorder.

XX OS Homo sapiens.

XX PN WO200183782-A2.

XX PD 08-NOV-2001.

XX PF 04-MAY-2001; 2001WO-US14431.

XX PR 04-MAY-2000; 2000US-201879P.

XX PA (SUGEN-) SUGEN INC.

XX PI Plowman GD, Whyte D, Sudarsanam S, Manning G, Caenepeel S;

XX PI Payne V;

XX DR WPI; 2002-041502/05.

XX DR N-PSDB; AAS97165.

XX Novel protease polypeptide useful for screening for substances that may
PT be used to treat, e.g., cancers, immune-related diseases,
PT cardiovascular disease, migraine, pain, psychotic and inflammatory
PT disorders -
XX
PS Claim 28; Figure 2A; 232pp; English.
XX
CC The invention relates to an isolated, enriched, or purified protease
CC polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to
CC screen for substances (S) that may modulate its activity. Administering
CC S (which modulates protease activity in vitro) may be used to treat a
CC disease or disorder selected from cancers (e.g., of tissues, of blood or
CC haematopoietic origin, of the breast, colon, lung, prostate, cervical,
CC brain, ovarian, bladder or kidney), immune-related diseases and
CC disorders, cardiovascular disease, brain or neuronal-associated diseases
CC (e.g., central or peripheral nervous system diseases, migraine, pain,
CC sexual dysfunction, mood disorders, attention disorders, cognition
CC disorders, hypotension, hypertension, psychotic disorders, neurological
CC disorders and dyskinesias), metabolic disorders and inflammatory
CC disorders. (I) may also be useful as a diagnostic tool for a disease or
CC disorder such as those above. AAU72876-AAU72910 represent human
CC protease amino acid sequences of the invention.
XX
SQ Sequence 234 AA;
XX
XX Query Match 31.6%; Score 427; DB 23; Length 234;
XX Best Local Similarity 39.7%; Pred. No. 1.9e-35;
XX Matches 102; Conservative 45; Mismatches 72; Indels 38; Gaps 7;
XX
QY 18 RYDMSGARLALTLCTVRAEGSEVDMALERMFRYLKFEETSKSDPTPAQOFLBEIDEFOQ 77
Db 1 QYDLSKARALLLVICORPAGOHDEVALGICWALGFETTRDPTPAQAFQELAQPRE 60
QY 78 TIDNWEPPVGCAPVVMAN-GEGLKGEDEKMYRLDELFLVANNKCKALRGKPKYIT 136
Db 61 QLDTCRGPVSCALVALMAHGGPRQLGADQEQVPELMQELS--RCQVLAQGRPKIFLL 118
QY 137 QACRGEHRDGC-----ELRGNBELGDEBELGDEVAVLKNNPOSIPYTDTLHI 186
Db 119 QACRGNRDAQVGPALPWTWSMURA-----PPSVPSHADVIOI 157
QY 187 YSTVEGYLSYRHDEKSGFIOTLTDPFIHKKG-SILELTEBITRLMANTVMOE--GKPR 243
Db 158 YAAQGVVAAR-DDKSGDFIQTIVELRANPGRDLLELTVNMRVCEQVGLPDCBELR 216
QY 244 KVMDEVOSTLRKLYLO 260
Db 217 KACLEIRSRRLRLCLQ 233
XX
XX RESULT 11
XX AAE00610
XX ID AAE00610 standard; Protein: 261 AA.
XX
XX AC AAE00610;
XX
XX DT 02-JUL-2001 (first entry)
XX
XX DE Chimeric cassette comprising human caspase with modified cleavage site.
XX
XX Human: caspase; beta-secretase; cleavage site; interdomain linker;
XX cysteine protease; apoptosis; caspase expression cassette; metastasis;
XX tumour; cathepsin B; urokinase; proliferation; gene therapy; chimera;
XX Alzheimer's disease.
XX
XX OS Chimeric - Homo sapiens.
XX
XX OS Chimeric - Unidentified.
XX
XX FH Key Location/Qualifiers
XX FT Region 1..147
XX FT /label= Caspase_large_subunit
XX FT Region 148..165

FT /note= "Beta-secretase cleavage site which replaces
FT the naturally occurring caspase cleavage site"
FT Region 165..261
FT /label= Caspase_small_subunit
XX
XX WO200129232-A2.
XX
XX 26-APR-2001.
XX
XX 19-OCT-2000; 2000MO-US28941.
XX
XX 20-OCT-1999; 99US-0160559.
XX
XX 14-AUG-2000; 2000US-0225564.
XX
XX (SCIO-) SCIOS INC.
XX
XX Cordell B, Li Y;
XX
XX WPI; 2001-290920/30.
XX
XX N-PSDB; AAD03918.
XX
XX Novel fusion polypeptide comprising first and second caspase subunit
XX separated by cleavage site not associated in nature with caspase
XX subunit, useful for cloning gene encoding enzymes involved in
XX proteolytic cleavage -
XX
XX Example 1; Fig 27; 116pp; English.
XX
XX The present amino acid sequence is an artificially engineered chimeric
XX cassette construct comprising human caspase-3 with interdomain linker
XX replaced by a Swedish mutant beta-secretase cleavage site. This modified
XX caspase-3 plays a pivotal role in Alzheimer's disease. Caspases are
XX a family of cysteine proteases, that participate in the initiation and
XX execution of apoptosis. Caspases exist as pro-enzymes, activated by
XX cleavage into a large and small subunit, occurring after specific
XX aspartic acid residues within the pro-enzyme sequence.
XX The present acid residues relates to a method for functional cloning of genes
XX encoding proteins or enzymes involved in proteolytic cleavage. The
XX invention is based on the use of caspase expression cassettes comprising
XX the coding sequence of a proteolytic cleavage site flanked by sequences
XX encoding two caspase subunit. A fusion polypeptide comprising a first
XX and a second caspase subunit, separated by a cleavage site not associated
XX in nature, is useful for cloning gene encoding enzymes involved in
XX proteolytic cleavage. An expression cassette containing fusion
XX polypeptide is used to identify a mutant cell line deficient in an
XX enzyme of interest and is also useful for diagnosis and suppression of
XX proliferation or metastases of a tumour cell characterised by
XX overexpression of a polypeptide (e.g. Cathepsin B or urokinase,
XX selectively expressed in the tumour cells). DNA encoding fusion
XX polypeptide is used in gene therapy.
XX
XX SQ Sequence 261 AA;
XX
XX Query Match 21.2%; Score 286.5; DB 22; Length 261;
XX Best Local Similarity 32.1%; Pred. No. 6.4e-21;
XX Matches 85; Conservative 41; Mismatches 104; Indels 35; Gaps 9;
XX
QY 16 EERYDMSGARLALTLCTV-----AREGSEVDMALERMFRYLKFEETSKMDPTA 65
Db 7 DNSYKMDYPEWGLCIILNNKMFHKSJGTMTSGTVDVAANLRERFRLKYEVNRKNDLTR 66
QY 66 QQFLEIDEFOQITIDNNEPVCAPV-VLMANHGEGLKGEDEGMVLEDFEVLNNKNC 124
Db 67 ---EBIVELMRDYSKSDHSGRSFVCLVSHGEGEIIFGNGP-VDDUKKITTFFRGDRC 121
QY 125 KALRGKPRVYIIQACRGEHRDPGEELRGNE--ELGCDDELGDEVAVLKNNPOSIPYTD 182
Db 122 RSLRGKPRKFLIQACRGTELDGCIETKTEISEVNLDAEPFHDMSACHK-----IPYAD 176
QY 183 TLHLYSTVEGYLSYRHDEKSGFIOTLTDPFIHKKGSIILELTEBITRLMANTVMOE 241
Db 177 FLVAYSTAPGYYSWRNSKDSWFIQSLC-AMLKQYADKLEPMHILTRV--NRKVAATEFES 233

QY 242 -----PRKVPNEVOSTLRKKLY 258
 Db 234 FSPDATFAKKQIPCIYVSMLTRKELY 258

RESULT 12
 ID ABB10110 standard; Protein; 452 AA.

AC ABB10110;

DE 26-JUL-2002 (first entry)

XX Mouse caspase 2 protein.

XX Caspase 2; antitense; cytosolic; osteopathic; cerebroprotective;
 KW neuroprotective; antilipemic; antiinflammatory; antimicrobial;
 KW haematopoietic disorder; bone metabolism disorder; cholesterol disorder;
 KW hyperproliferative disorder; cancer; blood disorder; stroke;
 KW brain injury; neurodegenerative disease; infection; inflammation;
 KW tumour.

XX Mus musculus.

PN WO200224720-A1.

XX 28-MAR-2002.

PF 14-SEP-2001; 2001WO-US28631.

XX 20-SEP-2000; 2000US-0667018.

PA (ISIS-) ISIS PHARM INC.

PI Zhang H, Watt AT;

XX WPI; 2002-351998/38.

DR N-PSDB; ABB58563.

PT New antisense compounds targeted to nucleic acid molecule encoding
 caspase 2, useful for treating diseases or conditions associated with
 caspase 2, e.g. cancer, blood disorders, stroke, brain injury and
 neurodegenerative diseases -
 PT neurodegenerative diseases -
 XX Example 13; Page 111-113; 146pp; English.

XX The invention relates to a compound 8-50 nucleobases in length targeted
 CC to a nucleic acid molecule encoding caspase 2, which specifically
 CC hybridises with and inhibits the expression of caspase 2, or specifically
 CC hybridises with at least an 8-nucleobase portion of an active site on a
 CC nucleic acid molecule encoding caspase 2. The activity of antisense
 CC oligonucleotides of the invention may be described as: cytostatic,
 CC osteopathic, cerebroprotective, neuroprotective, antilipemic,
 CC antiinflammatory and antimicrobial. The antisense compounds are useful
 CC for treating an animal having a disease or condition associated with
 CC caspase 2, such as haematopoietic disorder, bone metabolism disorder,
 CC cholesterol disorder, or a hyperproliferative disorder. These compounds
 CC may further be used as research reagents and diagnostics, to distinguish
 CC between functions of various members of a biological pathway, in the
 CC treatment of a disease or disorder which can be treated by modulating
 CC the expression of caspase 2, including cancer, blood disorders,
 CC stroke, brain injury and neurodegenerative diseases. They may also be
 CC used for prophylaxis, e.g. to prevent or delay infection, inflammation or
 CC tumour formation. The current sequence represents the mouse caspase 2
 CC protein.
 XX
 SQ Sequence 452 AA;

Query Match 20.5%; Score 276.5; DB 23; Length 452;
 Best Local Similarity 30.6%; Pred. No. 1.6e-19;
 Matches 71; Conservative 53; Mismatches 95; Indels 13; Gaps 6;

QY 36 REGSEVDMALERMFRYLKFEISTMKRDPPTAQOFLBEIDFQOCTIDNMEEPVSCAFVUMA 95

Db 219 RSGSDVHTTLVTLFKLGVNVAHVHDQTAQEMQKQNFQAQ-LPAAIRVYDSCV-VALLS 276
 QY 96 HGEELGLKGEDEKAVRLLEDLFEVLNNKCKALRGKPKVY11OACRGHRDPG---EELRG 152
 Db 277 HGVGGIGYGVGDKLLQLOEVRFLFDNANCPSLQNKPKMFFLOACRGDETBGVQDQGN 336
 QY 153 NEELGGDEELGGDEVAVLKNNPQISPTVYDTLHYSVVEGYLSYRHDEKSGF1QTLTDV 212
 Db 337 HTQSPGCEESDAGKEELMK--MRLPTRSDWICGACILGNAMNMTKRGSGWYIEALTQV 393
 QY 213 F1HKKG--ILLETBEITRLMANTENVMQEGK---RKVPNEVOSTLRKKLYL 259
 Db 394 FSERACDMHVAIDLKVALIKEREGYAPGTEFHRCKEMSEYCS1LCOQLYL 445

RESULT 13
 ID AAU05395 standard; Protein; 277 AA.

AC AAU05395;

XX 24-OCT-2001 (first entry)

DE Mouse caspase 3.

XX Mouse; caspase 3; apoptosis; hyperproliferative disorder; hepatitis;
 KW viral infection; haematopoietic disorder; autoimmune disorder;
 KW atherosclerosis; neurological disorder.

OS Mus musculus.

PN WO200153310-A1.

PD 26-JUL-2001.

PF 11-JAN-2001; 2001WO-US00888.

XX 18-JAN-2000; 2000US-0484617.

PA (ISIS-) ISIS PHARM INC.

PI Zhang H, Cowsett LM;

XX WPI; 2001-442252/47.

DR N-PSDB; AAS10510.

PT New antisense compound to inhibit caspase 3 is useful for treating
 PT hepatitis and atherosclerosis -
 XX Disclosure; Page 96-97; 127pp; English.

XX The present sequence representing mouse caspase 3 is described
 CC in an invention relating to novel antisense oligonucleotides
 CC (AAS10517-AAS10676) and methods of using these compounds for the
 CC modulation of caspase 3 expression. The caspase 3 antisense
 CC oligonucleotides specifically hybridise with and inhibit the
 CC expression of caspase 3. Antisense compounds targeted to caspase 3
 CC are useful to inhibit caspase 3 expression in cells or tissues and
 CC to modulate apoptosis. The caspase 3 antisense oligonucleotides are
 CC useful for treating disorders associated with expression of caspase 3.
 CC Such disorders include hyperproliferative disorders (e.g. cancer),
 CC viral infections (e.g. hepatitis), haematopoietic disorders, autoimmune
 CC disorders, atherosclerosis and neurological disorders (e.g. Alzheimer's
 CC disease).
 XX
 SQ Sequence 277 AA;

Query Match 20.4%; Score 276; DB 22; Length 277;
 Best Local Similarity 33.3%; Pred. No. 8.4e-20;
 Matches 79; Conservative 39; Mismatches 81; Indels 38; Gaps 9;

QY 35 AREGSEVDMALERMFRYLKFEISTMKRDPPTAQOFLBEIDFQOCTIDNMEEPVSCAFV-VL 93


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Db 63 SRGCTVDAAANLEETFGGLYQVANKNDLTREDLLEMD-----SVSKEDSKRSSFCVCI 118
Qy 94 MARGESGLKGEDEKAVRLDELFEVLNNKNCALRGKPKVYIIIOACRGEHRDPGEELRGN 153
Db 119 LSHGDEGVIVGTGNP-VELKKLTGFFRGDYCRSLTGKPKFIIOACGTETLDCIE---- 173
Qy 154 EELGDEELGDEVAVLKNNPQSIPTVDTLHLYSTVEGYLSYRHDEKSGGFIQTLTD-- 211
Db 174 TDSGTDEEMA-----CQKIPVEADFLYAVSTAPGYYSMNSKDGSWFIQSLCML 223
Qy 212 -VIRHKGSILLETETRLMANTENVQEGK-----PRKNEVOSTLRKKLY 258
Db 224 KLYAHK----LEFMHILTRV--NRKATFEFESFLDSTFPAKKOIPCIIVSMLTRELY 274

RESULT 14
AAR90703
ID AAR90703 standard; Protein; 435 AA.
AC AAR90703;
XX
XX
DT 10-APR-1996 (first entry)
DE Interleukin-1-beta converting enzyme like apoptosis protease-2.
XX
XX Interleukin-1-beta converting enzyme like apoptosis protease-2;
XX ICE-LAP-2; cell death; immunosuppression; AIDS; Alzheimer disease;
XX Parkinson disease; septic shock; rheumatoid arthritis; head injury;
XX antitumor; antiviral.
XX Homo sapiens.
XX MO9600297-A1.
XX
XX 04-JAN-1996.
XX
XX 23-JUN-1994; 94WO-US07127.
XX
XX 23-JUN-1994; 94WO-US07127.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Craig AR, Haeflins GA, Hudson PL, Kirkness EF, Wei WH;
XX
XX WPI: 1996-068881/07.
XX
XX N-PSDB; AAT15579.
XX
XX Interleukin-1 beta converting enzyme like apoptosis protease-1 and
XX PT -2 - controls programmed cell death, used in treatment of
XX PT immunosuppression related disorders, e.g. AIDS and Alzheimer's
XX PT disease
XX
XX Claim 1; Fig 2A-C; 58pp; English.
XX
XX Human interleukin-1-beta converting enzyme like apoptosis protease-2
XX CC (ICE-LAP-2) (AAR90703) is structurally related interleukin-1-beta
XX CC converting enzyme, which is responsible for apoptosis. Recombinant.
XX CC ICE-LAP-2 is obd. by expression of encoding cDNA (AAT15579) in
XX CC prokaryotic or eucaryotic host cells. It is used to treat diseases
XX CC related to abnormally controlled programmed cell death, to control
XX CC vertebrate development and tissue homeostasis, to overcome vital
XX CC infections and to treat immunosuppression-related disorders.
XX
XX
XX Sequence 435 AA;
XX
Query Match 20.4%; Score 275.5; DB 17; Length 435;
Best Local Similarity 29.6%; Pred. No. 1.9e-19;
Matches 68; Conservative 53; Mismatches 100; Indels 9; Gaps 4;
Qy 36 RESSEVDMEALMFRFLKFEESTMKRDPDPTAQOFLBELDEFQOITIDNMBEVSQAFVITMA 95
Db 202 RSGGDVHDSTLVTLFKLLGYDVHVLCDQTAQEMQEKLNFAQ-LPAHRYTDSQ-IVALLS 259

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Qy 96 HGEGLKGEDEKAVRLDELFEVLNNKNCALRGKPKVYIIIOACRGEHRDPGEELRGN 155
Db 260 HGVGAIYGVDSGLTLQAEVFOFLPDNANCPSLQNKPKMFMFIQACRGDETRGVNDQDGKN 319
Qy 156 LGGDEELGDEVAVLKNNPQSIPTVDTLHLYSTVEGYLSYRHDEKSGGFIQTLTDVFIH 215
Db 320 HAQSPGCEESDACKEXLPRKRLPTSPDMICGACLKGTAMRYTKRGSWYIEALQVF-S 378
Qy 216 KKGSILLETETRLMANTENVQEGKPR-----KVAPEVOSTLRKKLYL 259
Db 379 ERGDMHVAADLVKVALIKRREGYAPGTEFHRCKENSEVCSITLCRHL 428

RESULT 15
AAR66771
ID AAR66771 standard; Protein; 435 AA.
AC AAR66771;
XX
XX
DT 13-SEP-1995 (first entry)
DE Human interleukin-1 beta converting enzyme ced 3 homolog Ich-1(L).
XX
XX Human interleukin-1 beta converting enzyme ced 3 homolog; Ich-1(L);
XX KM oncogene bcl-2; programmed cell death; cancer treatment.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH Active-site 301..305
XX
XX MO9500160-A.
XX
XX 05-JAN-1995.
XX
XX 10-JUN-1994; 94WO-US06630.
XX
XX 24-JUN-1993; 93US-0080850.
XX
XX (GCHO) GEN HOSPITAL CORP.
XX
XX Miura M, Yuan J;
XX
XX WPI: 1995-051742/07.
XX
XX N-PSDB; AAO79971.
XX
XX Promoting or preventing programmed cell death in vertebrate cells
XX PT - by inhibiting the activity of interleukin-1 beta converting
XX PT enzyme.
XX
XX Example 5; Fig 12A; 116pp; English.
XX
XX AAO79971 encodes AAR66771 human interleukin-1 beta converting enzyme
XX CC ced 3 homolog Ich-1(L), increasing Ich-1(L)'s enzymatic activity can
XX CC promote the programmed cell death of cancer cells (pref. those
XX CC overexpressing the bcl-2 oncogene), this can be used as the basis
XX CC of a new cancer treatment. Alternatively by reducing Ich-1(L)'s
XX CC enzymatic activity programmed cell death can be inhibited, this may
XX CC be useful in the development of new cell lines which remain viable in
XX CC culture for extended or indefinite periods, independant of growth
XX CC factors.
XX
XX
XX Sequence 435 AA;
XX
Query Match 20.3%; Score 274.5; DB 16; Length 435;
Best Local Similarity 29.7%; Pred. No. 2.4e-19;
Matches 68; Conservative 51; Mismatches 103; Indels 7; Gaps 4;
Qy 36 RESSEVDMEALMFRFLKFEESTMKRDPDPTAQOFLBELDEFQOITIDNMBEVSQAFVITMA 95
Db 202 RSGGDVHDSTLVTLFKLLGYDVHVLCDQTAQEMQEKLNFAQ-LPAHRYTDSQ-IVALLS 259

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OY  HGEGLLKGEDEKXVRLIEDLEVLNNKXCKYLRKPKYIIIOACRGHNRPGEEILKONEE 155
Dy  260 HGVEAATIGVGVSKLLQLOLEVVFLPNNACPSLONKKPKPFIIQACRGEDTRGVDDQDGKN 319
Oy  156 LGGDEELGGDEVAALVKNNPQSIPTUTDRLAHYSTVEGYLSYRHEKSGSFYQTLTDVFIH 215
Dy  320 HAGSGCCESDAGKEKLPKXMLPLTRSDMTCGYALCKLGAANRNKTRKRSWIETALAQVFSE 379
Oy  216 KKGSG--ILELTEETIRLMANTEVNOEGRP--RKVNEPVOSTLRKKLYL 259
Dy  380 RACDMHVAADMLVKVALLKDRBGVARGTGFPRKCKEMSEYCTGLCRHLYL 428

```

Search completed: February 26, 2003, 12:19:02
Job time : 35.1474 secs

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: February 26, 2003, 12:17:56 : Search time 13.9841 Seconds
(without alignments)
547.048 Million cell updates/sec

Title: US-09-989-903-2

Perfect score: 1350
Sequence: 1 KPMESEMSDPQLOERYD.....KPRKNPEVOSTLRKLYLQ 260Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1a1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1350	100.0	260	US-09-187-789-2	Sequence 2, Appl
2	1350	100.0	260	US-09-139-600-2	Sequence 2, Appl
3	934.5	69.2	242	US-09-187-789-5	Sequence 5, Appl
4	804.5	59.6	214	US-09-187-789-9	Sequence 9, Appl
5	692.5	51.3	230	US-09-187-789-7	Sequence 7, Appl
6	384	28.4	74	US-09-187-789-63	Sequence 63, Appl
7	384	28.4	74	US-09-139-600-58	Sequence 58, Appl
8	299	22.1	56	US-09-187-789-54	Sequence 64, Appl
9	299	22.1	56	US-09-139-600-59	Sequence 59, Appl
10	280	20.7	53	US-09-187-789-65	Sequence 65, Appl
11	280	20.7	53	US-09-139-600-60	Sequence 60, Appl
12	275.5	20.4	435	PCT-US94-07127A-4	Sequence 4, Appl
13	274.5	20.3	421	US-08-983-502-10	Sequence 10, Appl
14	274.5	20.3	421	PCT-US96-10521-10	Sequence 10, Appl
15	274.5	20.3	435	US-08-258-287B-53	Sequence 53, Appl
16	274.5	20.3	435	US-08-368-704C-51	Sequence 51, Appl
17	274.5	20.3	435	US-09-561-756-9	Sequence 9, Appl
18	274.5	20.3	435	US-09-227-721-9	Sequence 9, Appl
19	274.5	20.3	435	US-08-816-075-2	Sequence 2, Appl
20	274.5	20.3	441	US-08-258-287B-44	Sequence 44, Appl
21	274.5	20.3	441	US-08-368-704C-43	Sequence 43, Appl
22	274.5	20.3	277	US-08-890-542A-2	Sequence 2, Appl
23	274.5	20.3	277	US-08-591-605-2	Sequence 2, Appl
24	274.5	20.3	277	US-08-964-308-6	Sequence 6, Appl
25	274.5	20.3	277	US-08-462-969B-4	Sequence 4, Appl
26	274.5	20.3	277	US-08-964-313-6	Sequence 6, Appl
27	274.5	20.3	277	US-09-069-138-6	Sequence 6, Appl

28	273	20.2	277	4	US-09-561-756-12	Sequence 12, Appl
29	273	20.2	277	4	US-09-227-721-12	Sequence 10, Appl
30	273	20.2	277	4	US-08-983-502-30	Sequence 30, Appl
31	273	20.2	277	5	PCT-US96-10521-30	Sequence 30, Appl
32	265	19.6	503	3	US-08-258-287B-36	Sequence 36, Appl
33	265	19.6	503	3	US-08-368-704C-36	Sequence 36, Appl
34	264	19.6	277	3	US-08-964-313-10	Sequence 10, Appl
35	264	19.6	277	3	US-08-964-313-10	Sequence 10, Appl
36	264	19.6	277	4	US-09-069-138-10	Sequence 37, Appl
37	263.5	19.5	477	3	US-08-258-287B-37	Sequence 37, Appl
38	263.5	19.5	477	3	US-08-368-704C-37	Sequence 37, Appl
39	259	19.2	505	2	US-08-394-189B-5	Sequence 5, Appl
40	259	19.2	505	5	PCT-US93-05701-20	Sequence 5, Appl
41	259	19.2	505	5	PCT-US93-05705-5	Sequence 5, Appl
42	255.5	18.9	303	4	US-09-561-756-24	Sequence 24, Appl
43	255.5	18.9	303	4	US-09-227-721-24	Sequence 24, Appl
44	255.5	18.9	303	4	US-08-556-627A-2	Sequence 2, Appl
45	253	18.7	416	3	US-08-852-936C-1	Sequence 1, Appl

ALIGNMENTS

```
RESULT 1
US-09-187-789-2
Sequence 2, Application US/09187789.
Patent No. 6340740.
GENERAL INFORMATION:
APPLICANT: Fernandez, Emdad S.
APPLICANT: Fernandez-Alnemati, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187, 789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 260
TYPE: PRT
ORGANISM: Mus musculus
US-09-187-789-2

Query Match      100.0%; Score 1350; DB 4; Length 260;
Best Local Similarity 100.0%; Pred No. 5 6e-135;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPMESEMSDPQLOERYDMSGARLALTLCTKAREGSEVDMELERFYLKFESTMK 60
D 1 KPMESEMSDPQLOERYDMSGARLALTLCTKAREGSEVDMELERFYLKFESTMK 60
QY 61 RDPFNOQFLERLDFFOOTIDWMEPVSQAFVVLMAHGEGLKGEDEDMVRLLEDFEVLN 120
D 61 RDPFNOQFLERLDFFOOTIDWMEPVSQAFVVLMAHGEGLKGEDEDMVRLLEDFEVLN 120
QY 121 NKNCKALRGKRVYIIQACRGEHRDPGBELRGNEELGDEELGDEVAVLKNNPOSIPY 180
D 121 NKNCKALRGKRVYIIQACRGEHRDPGBELRGNEELGDEELGDEVAVLKNNPOSIPY 180
QY 181 TDTLHIVSYVGVLYSRHDEKSGFIOTLTVDFTHKKSIIELTEITRLMANTVMEQG 240
D 181 TDTLHIVSYVGVLYSRHDEKSGFIOTLTVDFTHKKSIIELTEITRLMANTVMEQG 240
QY 241 KPRKNPEVOSTLRKLYLQ 260
D 241 KPRKNPEVOSTLRKLYLQ 260

RESULT 2
US-09-139-600-2
Sequence 2, Application US/09139600
Patent No. 6432628
GENERAL INFORMATION:
```

```

; APPLICANT: Alnemri, Emdad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHOD OF USE
; FILE REFERENCE: 480140.434
; CURRENT APPLICATION NUMBER: US/09/139,600
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-139-600-2

```

```

Query Match          100.0%; Score 1350; DB 4; Length 260;
Best Local Similarity 100.0%; Pred. No. 5.6e-135;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 KPDSEMSDPOLOERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKESTWK 60
Db 1 KPDSEMSDPOLOERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKESTWK 60
Qy 61 RDPTRQOFLIEIDFQOITIDNMEEPVSCAFVVLMAHGEGLKGEDEKVRLEDLFEVLN 120
Db 61 RDPTRQOFLIEIDFQOITIDNMEEPVSCAFVVLMAHGEGLKGEDEKVRLEDLFEVLN 120
Qy 121 MNCKALGKPKVYIIQACRGHRDGEELRGNEELGDEELGDEVANLKNPQISPT 180
Db 121 MNCKALGKPKVYIIQACRGHRDGEELRGNEELGDEELGDEVANLKNPQISPT 180
Qy 181 TDTLHIVSTVEGYSYRHDGSGFIQTLTDVFIHKKSILTEITRLMANTVMOEG 240
Db 181 TDTLHIVSTVEGYSYRHDGSGFIQTLTDVFIHKKSILTEITRLMANTVMOEG 240
Qy 241 KPRKVNPEVOSTLRKKLYIQ 260
Db 241 KPRKVNPEVOSTLRKKLYIQ 260

```

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RESULT 3
US-09-187-789-5
; Sequence 5, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emdad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-187-789-5

```

```

Query Match          69.2%; Score 934.5; DB 4; Length 242;
Best Local Similarity 70.9%; Pred. No. 5.2e-91;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;

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```

Qy 8 MSDPPOLOERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKESTWK 67
Db 1 MSNPRLSEBEKYMDSGARLALTLCVTKAREGSEVDMEALERMFRYLKESTWK 60
Qy 68 FLEELDEFQOITIDNMEEPVSCAFVVLMAHGEGLKGEDEKVRLEDLFEVLN 127
Db 61 FOELEKFOQALDSREDPVSCAFVVLMAHGRGFLKGEDEVVKLENLEALNNKNCAL 120
Qy 128 RGPVKVYIIQACRGHRDGEELRGNEELGDEELGDEVANLKNPQISPT 186

```

```

Db 121 RAKPKVYIIQACRGHRDGP-----ETVGGDEIVWVINDSPQITPTTDLAHV 168
Qy 167 YSTVEGYLSYRHDGSGFIQTLTDVFIHKKSILTEITRLMANTVMOEGKPRKVN 246
Db 169 YSTVEGYIAYRRDQSGCFIQTLTDVFTKRKGHIELLTVTRMAEALVQEGKARTN 228
Qy 247 PEVOSTLRKKLYIQ 260
Db 229 PEIOSTLRKKLYIQ 242

```

```

RESULT 4
US-09-187-789-9
; Sequence 9, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emdad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-187-789-9

```

```

Query Match          59.6%; Score 804.5; DB 4; Length 214;
Best Local Similarity 63.0%; Pred. No. 2.6e-77;
Matches 160; Conservative 27; Mismatches 26; Indels 41; Gaps 3;

```

```

Qy 8 MSDPPOLOERYDMSGARLALTLCVTKAREGSEVDMEALERMFRYLKESTWK 67
Db 1 MSNPRLSEBEKYMDSGARLALTLCVTKAREGSE----- 34
Qy 68 FLEELDEFQOITIDNMEEPVSCAFVVLMAHGEGLKGEDEKVRLEDLFEVLN 127
Db 35 --EELEKFOQALDSREDPVSCAFVVLMAHGRGFLKGEDEVVKLENLEALNNKNCAL 92
Qy 128 RGPVKVYIIQACRGHRDGEELRGNEELGDEELGDEVANLKNPQISPT 186
Db 93 RAKPKVYIIQACRGHRDGP-----ETVGGDEIVWVINDSPQITPTTDLAHV 140
Qy 187 YSTVEGYLSYRHDGSGFIQTLTDVFIHKKSILTEITRLMANTVMOEGKPRKVN 246
Db 141 YSTVEGYIAYRRDQSGCFIQTLTDVFTKRKGHIELLTVTRMAEALVQEGKARTN 200
Qy 247 PEVOSTLRKKLYIQ 260
Db 201 PEIOSTLRKKLYIQ 214

```

```

RESULT 5
US-09-187-789-7
; Sequence 7, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emdad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 230

```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-187-789-7

```

Query Match	51.3%	Score 692.5;	DB 4;	Length 230;
Best Local Similarity	72.0%	Pred. No. 2.1e-65;		
Matches 134; Conservative	22;	Mismatches 17;	Indels 13;	Gaps 2;

Qy	8	MSDQPOLOEEFYDMSGARLALTLCTVKARSESEYDMALTEMFYLKJESSTMKSDPTAQO	6
Db	1	MSNRSLSEEEKYDMSGARLALTLCTVKARSESEEDLDALHMFQOLKRESSTMKSDPTAQO	60
Qy	68	FLEELDEFQOTIDNMEEBVSCAFVILMAHGEGLKGDDEKXVRLEDLFEVLNNKCKAL	127
Db	61	FOELELEKFOALIDSRDEDPVSCAFVILMAHGREGLKGDGEMVKLEENFEALNNKNCQAL	120
Qy	128	RGRKRVYIIQACRGRHRDPGEELKAGNEBLGSDDEELGDE-VAVLKNNQPSLPTTDLTLHI	186
Db	121	RAKRVYIIQACRGRBQRDPG-----ETVGGDEIMVLIKDSQPOTLPTYTDALHV	166
Qy	187	YSTVEG	192
Db	169	YSTVEG	174

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RESULT 6
US-09-187-789-63
; Sequence 63, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434c1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-187-789-63

```

```

Query Match: 28.4%; Score 384; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY      35  ARGESEVDMEALERMFRFYLLKFESTMRKRDPTAAQFLLELDEFOOTIDNNEEPVSCAFVLM 94
      |||
Db       1  ARRESVDMDALERMFRFYLLKFESTMRKRDPTAAQFLLELDEFOOTIDNNEEPVSCAFVLM 60
QY      95  AHGEGGLLKGEDEK 108
      |||
Db       61  AHGEGGLLKGEDEK 74

RESULT 7
US-09-139-600-58
Sequence 58, Application US/09139600
Patent No. 6432628
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434
CURRENT APPLICATION NUMBER: US/09/139,600
CURRENT FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 58

```

```

; LENGTH: 74
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-139-600-58

```

Query Match	28.4%	Score 384	DB 4	Length 74
Best Local Similarity	100.0%	Pred. No. 1.8e-33		
Matches 74	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	95	61
ARGSEVDMEALERFRFYLKPESTWKRPDPTAQOFLBELDEFOQTIDNWEPPVSCAFVILM	ARGSEVDMEALERFRFYLKPESTWKRPDPTAQOFLBELDEFOQTIDNWEPPVSCAFVILM	ARGSEVDMEALERFRFYLKPESTWKRPDPTAQOFLBELDEFOQTIDNWEPPVSCAFVILM
1	1	1
60	60	60

```

; RESULT 8
; US-09-187-789-64
; Sequence 64, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 64
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-187-789-64

```

QY	109	MVRLEDLEFVANNOCCKALRGKPRVYIIIOARGGHRDPSGEEELRGNEELGSGDEELGCG	164
Db	1	MVRLEDLEFVANNOCCKALRGKPRVYIIIOARGGHRDPSGEEELRGNEELGSGDEELGCG	56
		Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
		Query Match 22.1%; Score 299; DB 4; Length 56;	
		Best Local Similarity 100.0%; Pred. No. 1.2e-24;	
		Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

```

? RESULT 9
? US-09-139-600-59
? Sequence 59, Application US/09139600
? Patent No. 6432628
? GENERAL INFORMATION:
? APPLICANT: Alnemri, Emad S.
? APPLICANT: Fernandez-Alnemri, Teresa
? TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE,
? TITLE OF INVENTION: AND METHOD OF USE
? FILE REFERENCE: 480140.434
? CURRENT APPLICATION NUMBER: US/09/139,600
? CURRENT FILING DATE: 1998-08-25
? NUMBER OF SEQ ID NOS: 65
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 59
? LENGTH: 56
? TYPE: PRT
? ORGANISM: Mus musculus
? US-09-139-600-59

```

```

Query March      22.1%; Score 299; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.2e-24;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 109 MVRLEDTPEVANNNNCKALRGKPKRYITIAQRGEHRDPEELLRGNNEELGSDPELGG 164
|||||

```

Db 1 MWLEDLFEVLNNKCKALRGKPKVYIIQACRGHEHDPGEELRGNEELGDBELG 56

RESULT 10

US-09-187-789-65

Sequence 65, Application US/09187789

Patent No. 6340740

GENERAL INFORMATION:

APPLICANT: Alnemri, Emed S.

APPLICANT: Fernandez-Alnemri, Teresa

TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING

TITLE OF INVENTION: AND METHODS OF USE

FILE REFERENCE: 480140.434C1

CURRENT APPLICATION NUMBER: US/09/187,789

CURRENT FILING DATE: 1998-11-06

NUMBER OF SEQ ID NOS: 78

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 65

LENGTH: 53

TYPE: PRT

ORGANISM: Mus musculus

US-09-187-789-65

Query Match 20.7%; Score 280; DB 4; Length 53;

Best Local Similarity 100.0%; Pred. No. 1.1e-22;

Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 165 DEVALKNNPQSIPTTDLHTSYVEGYLSYRHEKSGSFTOTLTDVFIHKK 217

1 DEVALKNNPQSIPTTDLHTSYVEGYLSYRHEKSGSFTOTLTDVFIHKK 53

RESULT 11

US-09-139-600-60

Sequence 60, Application US/09139600

Patent No. 6432628

GENERAL INFORMATION:

APPLICANT: Alnemri, Emed S.

APPLICANT: Fernandez-Alnemri, Teresa

TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING

TITLE OF INVENTION: AND METHOD OF USE

FILE REFERENCE: 480140.434

CURRENT APPLICATION NUMBER: US/09/139,600

CURRENT FILING DATE: 1998-08-25

NUMBER OF SEQ ID NOS: 65

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 60

LENGTH: 53

TYPE: PRT

ORGANISM: Mus musculus

US-09-139-600-60

Query Match 20.7%; Score 280; DB 4; Length 53;

Best Local Similarity 100.0%; Pred. No. 1.1e-22;

Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 165 DEVALKNNPQSIPTTDLHTSYVEGYLSYRHEKSGSFTOTLTDVFIHKK 217

1 DEVALKNNPQSIPTTDLHTSYVEGYLSYRHEKSGSFTOTLTDVFIHKK 53

RESULT 12

PCT-US94-07127A-4

Sequence 4, Application PC/TUS9407127A

GENERAL INFORMATION:

APPLICANT: HE, ET AL.

TITLE OF INVENTION: Interleukin-1 Converting Enzyme Like Apoptosis Protease-1, an

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

ADDRESSEE: CECCHI, STEWART & OLSTEIN

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/07127A

FILING DATE: submitted herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: FERRARO, GREGORY D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-184

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 435 AMINO ACIDS

TYPE: AMINO ACID

STRANDEDNESS:

TOPOLOGY: LINEAR 2

MOLECULE TYPE: PROTEIN

PCT-US94-07127A-4

Query Match 20.4%; Score 275.5; DB 5; Length 435;

Best Local Similarity 29.6%; Pred. No. 8.3e-21;

Matches 68; Conservative 53; Mismatches 100; Indels 9; Gaps 4;

Db 36 REGSEVDMEALERNFRYKKESTMKRDPFAOQFLBELDEFQOTIDNMEEPVSCAFVYIMA 95

202 RSGGDVDSHTLVTLFKLGGDVHVLCDPTAOEMOEKLNFAQ-LPAHRTVDS-C-IVALLS 259

Db 96 HGEELKGEDEKVRLEDLFEVLNNKCKALRGKPKVYIIQACRGHEHDPGEELRGNEE 155

260 HGEBAIVGVGKLLQAEVFLPDNANCPSLQNKPKVFIQACRGDETDGVDQDQGN 319

Db 165 LGDBELGDBAVAVLKNPQSIPTTDLHTSYVEGYLSYRHEKSGSFTOTLTDVFIH 215

320 HAGSPGCEESDAGKEKLPKMLPTRSDMICYACLCGTAAMRNKRKGSWYIEALAQV-S 378

Db 216 KKGSLLEETETRLMANTEVMOEGKPR-----KVNPEVOSTLRKKLYL 259

379 ERGCDMIVADMVLVKVNALIKDREGVAPGTEPRCKEMSEYVCTLCRHLYL 428

RESULT 13

US-08-963-502-10

Sequence 10, Application US/08963502

Patent No. 6399327

GENERAL INFORMATION:

APPLICANT: David WALLACH

APPLICANT: Mark P. BOLDIN

APPLICANT: Tanya M. GONCHAROV

APPLICANT: Yuri V. GOLTSEV

TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF PAS RECEPTORS

TITLE OF INVENTION: AND OTHER PROTEINS

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Browdy and Neimark

STREET: 419 Seventh Street N.W., Ste. 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

FILING DATE: 10-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/080,850
FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609,3920001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
TELEX: 248636 SSR
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-258-287B-53

Query Match 20.3%; Score 274.5; DB 3; Length 435;
Best Local Similarity 29.7%; Pred. No. 1.1e-20;
Matches 68; Conservative 51; Mismatches 103; Indels 7; Gaps 4;
QY 36 REGSEVDMEALERMFRYLKFEISTMKRDPPTAQOFLLEDDEPQOTIDNWEESPVSQAFVILMA 95
DB 202 RSGGVDVHSTLVTLFKLGYDVHVLCDOTAQEMOEKLNFAQ-LPAHRTDSC-IVALLS 259
QY 96 HGEGLKGEDEKAVRLDELFEVLNNKCKALRGKPKVYIIQACGGEHRDPGEELRGNEE 155
DB 260 HGVEGAIYGVGDKLQLQDEVFQLPDNANCPSLQNKPKMFFIQACRGDETDRCGVDOODGKN 319
QY 156 LCGDEELGDEVAVALKNNPQSIPTYDTLHISTVEGYLSVRHDEKSGSGLIOTLTDVFIH 215
DB 320 HAGSPGCEESDGKKEKLPKMRLLPTRSDMTCGYACLKGTAMKRNTRGSGWYIEALQVFESE 379
QY 216 KKGS--ILELTEITRLMANTFVMOEGKP---RYNPEVQSTLRKKLYL 259
DB 380 RACDWHVADMLVKVNAALIKDREGYAPGTEFHRCKEMSEYCSLCHNLVL 428

Search completed: February 26, 2003, 12:22:03
Job time: 14.9841 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 26, 2003, 12:16:30 ; Search time 27.9681 Seconds
(without alignments)
1915.475 Million cell updates/sec

Title: US-09-989-903-2
Perfect score: 1350
Sequence: 1 KPDMSEMSDPQLQGEERYD.....KPKKNPEVQSTLRKKLYIQ 260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp archaea:*
2: sp bacteria:*
3: sp fungi:*
4: sp human:*
5: sp invertebrate:*
6: sp mammal:*
7: sp mhc:*
8: sp organelle:*
9: sp phage:*
10: sp plant:*
11: sp rodent:*
12: sp virus:*
13: sp vertebrate:*
14: sp unclassified:*
15: sp virus:*
16: sp bacteriap:*
17: sp archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	295.5	21.9	423	13	Q91B67
2	278	20.6	318	13	Q91B65
3	278	20.6	403	13	Q90WU0
4	276	20.4	220	11	Q90W14
5	274.5	20.3	435	4	Q9BUP7
6	274.5	20.3	452	11	O55194
7	274	20.3	277	4	Q96A51
8	273	20.2	277	6	Q95ND5
9	272	20.1	277	4	Q96KP2
10	266	19.7	282	13	Q98UI8
11	265	19.7	454	11	Q98GT0
12	264.5	19.6	303	11	O88550
13	257	19.0	416	4	Q9B062
14	255	18.9	454	11	Q9JHK1
15	254	18.8	399	13	Q91B63
16	253	18.7	283	13	Q93417

17	252	18.7	302	13	Q91B59	Q91B59 oncorhynch
18	246	18.2	182	6	O77623	O77623 ovis aries
19	245.5	18.2	476	13	Q91B33	Q91B33 brachydanto
20	242	17.9	480	11	O89110	O89110 m caspase 8
21	241	17.9	304	11	Q93415	Q93415 gallus gall
22	241	17.9	482	11	Q9JHX4	Q9JHX4 rattus norv
23	240.5	17.8	293	4	Q9BQ67	Q9BQ67 homo sapien
24	240.5	17.8	520	13	Q91B62	Q91B62 xenopus lae
25	238	17.6	417	5	Q9YIU6	Q9YIU6 pristionchu
26	237	17.6	276	11	Q9D089	Q9D089 mus musculu
27	234.5	17.4	482	13	Q90WU1	Q90WU1 gallus gall
28	234	17.3	276	11	Q99M47	Q99M47 mus musculu
29	233.5	17.3	277	11	O35397	O35397 rattus norv
30	232	17.2	383	13	Q91B17	Q91B17 brachydanto
31	229	17.0	283	13	O42284	O42284 gallus gall
32	227	16.8	500	13	Q91B64	Q91B64 xenopus lae
33	223	16.5	326	5	Q9GV88	Q9GV88 hydra atten
34	222	16.4	496	4	Q9COK4	Q9COK4 homo sapien
35	220	16.3	538	4	O8TD15	O8TD15 homo sapien
36	219	16.2	303	13	Q91B66	Q91B66 xenopus lae
37	215.5	16.0	308	5	Q9NHP9	Q9NHP9 drosophila
38	215.5	16.0	308	5	Q9VET9	Q9VET9 drosophila
39	213.5	15.8	479	4	O8WT08	O8WT08 homo sapien
40	209	15.5	393	11	Q9R0S9	Q9R0S9 mus musculu
41	206	15.3	402	11	Q91W32	Q91W32 rattus norv
42	205.5	15.2	347	5	Q9GV89	Q9GV89 hydra atten
43	203	15.0	373	11	Q91XW7	Q91XW7 rattus norv
44	200	14.8	420	11	Q920D5	Q920D5 rattus norv
45	196	14.5	404	13	Q9DDJ2	Q9DDJ2 brachydanto

ALIGNMENTS

RESULT 1
ID Q91B67 PRELIMINARY; PRT; 423 AA.
AC Q91B67;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Caspase-2.
GN XCASPASE-2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N. A.
RX MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yaeita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
family";
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL: AB038168; BAA94746.1; -;
DR HSPR: P29466; 1ICE.
DR MEROPS: C14.006; -;
DR InterPro: IPR001315; CARD.
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00655; ICE_P10; 1.
DR Pfam: PF00656; ICE_P20; 1.
DR PRINTS: PRO0376; IL1BCENZME.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00115; CASc; 1.
DR PROSITE: PSS0209; CARD; 1.
DR PROSITE: PSS0122; CASPASE_CYS; 1.
DR PROSITE: PSS0121; CASPASE_HIS; 1.
DR PROSITE: PSS0207; CASPASE_P10; 1.
DR PROSITE: PSS0208; CASPASE_P20; 1.

SQ SEQUENCE 423 AA; 47123 MW; E91EBJFD13F01FD CRC64;
 Query Match 21.9%; Score 295.5; DB 13; Length 423;
 Best Local Similarity 27.0%; Pred. No. 2.7e-16;
 Matches 84; Conservative 58; Mismatches 104; Indels 65; Gaps 10;
 QY 2 PDMESEMSDP-----OPLQEEERYDMSGARLALTLTLC-----VTKARE----- 37
 DB 114 PQVESTLSRPGHQICREYREESIDDDGDPVTLQCGVNFYITHCQAYKMHSCPRGRL 173
 QY 38 -----GSEVDMALERMFRYLKFESTMKDPHTAQQLLELDEFQQTIDMW 82
 DB 174 ISNVKFEPPDLRYCGGGEVLDLASLETLFSSLSGQVAVRCNLNAQSMQSLGAFSAL---- 229
 QY 83 EEPVSCAF-----VLMAGHEEGLTKGEDKMYRLIEDLFEVLNNKNCKALRGKPKVYIQA 138
 DB 230 --PVHSALDSCVVALISHLDGAVYTGDKTLVQLQGVFALDINAHPQIQNPKMFIIQA 287
 QY 139 CGEHRDPGEELRGNEELG-----DEELGDEVAVLKNNPOSIPYTDLTHTYSTVEGY 193
 DB 288 CGEETDRGVQDRDGEQSGSPCEQSDAGREDIKV-----RLPTQSDMICAYACKTGT 341
 QY 194 LSYRDEKSGSGFIQTLTDVFI-HKKS-LLELTETRLMANTVWQEGKP---RVNPE 248
 DB 342 VSLRNTKRSWVQDLVSVFSQHSKDTHVADMLKVNALIKEREGHAPGTEFHRCKEMSE 401
 QY 249 VOSTLRKKLYL 259
 DB 402 YCSTLCRDLYL 412

RESULT 2
 ID Q91B65 PRELIMINARY; PRT; 318 AA.
 AC Q91B65:
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Caspase-7.
 GN XCASPASE-7.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20209426; PubMed=10744739;
 RA Nakajima K., Takahashi A., Yaoita Y.;
 RT "Structure, expression and function of the Xenopus laevis caspase
 family";
 RL J. Biol. Chem. 275:10484-10491(2000).
 DR EMBL; AB038170; BAA94748.1; --.
 DR HSSP; P42574; IPAD.
 DR MEROPS; C14.004; --.
 DR InterPro; IPR002398; ICE.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR Pfam; PF00655; ICE_p10; 1.
 DR Pfam; PF00656; ICE_p20; 1.
 DR PRINTS; PR00376; ILBENZYM.
 DR SMART; SM00115; CASG; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 SQ SEQUENCE 318 AA; 35937 MW; 6EB06684AF86A128 CRC64;

Query Match 20.6%; Score 278; DB 13; Length 318;
 Best Local Similarity 32.9%; Pred. No. 5.2e-15;
 Matches 77; Conservative 39; Mismatches 96; Indels 22; Gaps 7;
 QY 35 AREGSEVDMALERMFRYLKFESTMKRDPHTAQQLLELDEFQQTIDMWEPVSCAFV-VL 93

DB 97 ANGTIDIDARELLRCFKGIGFVNVYNNKSC---EEMENLRTVAQODHKDSACFACIF 152
 QY 94 MHAGEGLTKGEDKMYRLIEDLFEVLNNKNCKALRGKPKVYIQA CGEHRDPGELGN 153
 DB 153 LSHGEGGLYIGTGAM-PKVLTTLPFGDNCRLVLGKRPFLIQACRGHEPDDG----- 205
 QY 154 BELGDEBELGDEVAVLKNNPOSIPYTDLTHTYSTVEGYLSYRDEKSGSGFIQTLTDVF 213
 DB 206 --LEADSGSVNDSLETPDANPRHKIPEVADFLVYSTVEGYLSWRNPGMSWVQALCSV- 262
 QY 214 IHKKSILELTETRLMANTVWQEGKP---RVNPEVOSTLRKKLYLQ 260
 DB 263 INEYKELEVMQILTRVNFVLTATQEPESYSDPQFSKKQIPCVSMILTELYFK 316

RESULT 3
 ID Q90WU0 PRELIMINARY; PRT; 403 AA.
 AC Q90WU0:
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Caspase 9 (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Barton S., Bridgham J.T., Johnson A.L.;
 RT "Caspase-8 and -9 expression in the hen ovary";
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY057940; AAL23701.1; --.
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00655; ICE_p10; 1.
 DR Pfam; PF00656; ICE_p20; 1.
 DR PROSITE; PS50209; CARD; 1.
 DR PROSITE; PS01122; CASPASE_CYS; UNKNOWN_1.
 DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
 FT NON_TER
 SQ SEQUENCE 403 AA; 44913 MW; 0F1E40C3E6594FC4 CRC64;

Query Match 20.6%; Score 278; DB 13; Length 403;
 Best Local Similarity 28.2%; Pred. No. 7e-15;
 Matches 87; Conservative 44; Mismatches 106; Indels 72; Gaps 9;
 QY 1 KPDMSEMSDPOLQEEERYDMSGARLALTLTLC-----TKAREGSE 40
 DB 112 QPESERFRMPAPAGSANDKSRPTDWCTSCQGTCPGCHLIPNNVSPSRDSDLSTRASD 171
 QY 41 VDMALERMFRYLKFESTMKRDPHTAQQLLELDEFQQTIDMWEEPVSCAFVLMAGHEE 99
 DB 172 ICEKLEKRFSLCFHVRLRLKAQEIIDVELRLAR-LDH--SALDCCLVYLISHGCT 228
 QY 100 -----GLKGEDEKMYRLIEDLFEVLNNKNCKALRGKPKVYIQA CGEHRDPGEL--- 150
 DB 229 SHIOPGGYIGTGKTIPIERLVNFFNSQCSLKGKRLPFIQACGGEQKQGEVQCE 288
 QY 151 -----RGNEELGDEBELGDEVAVLKNNPOSIPYTDLTHTYST 189
 DB 289 SPQDETCSRISDAILPQAPSGNE---DEP---DAYA-----SLTPGDILVYST 334
 QY 190 VEGYLSYRDEKSGSGFIQTLTDVFIHKKSILELTETRLMANTVWQEGKPKVNPPEV 249

ID	Q90M14	PRELIMINARY;	PRT;	220 AA.
DB	335	PF6F5WMDKXSGSVYVERLDSVLEHYARS----	EDLTLKLARVSDIYSKRRYKQIFGC	390
Oy	250	OSTLRKKLY 258		
Db	391	FNFLRKIF 399		
RESULT 4				
ID	Q90M14	PRELIMINARY;	PRT;	220 AA.
AC	Q90M14;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Cp332 Apoptotic protease (Fragment).			
GN	CASP3.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RP	SEQUENCE FROM N.A.			
RA	Dentis F., Alam A., Cohen L., Hartgers F., Braun M., Martinez O.,			
RA	Fortin J.-P., Sekaly R.-P.:			
RT	"Multiple Pathways of Apoptosis Converging on the Cp332 Protease."			
RL	Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; U63720; AAD09504.1; -			
DR	HSSP; P42574; IPAU.			
DR	MEROPS; C14.003; -			
DR	MCD; MG1.107739; Caep3.			
DR	InterPro; IPR002398; ICE.			
DR	InterPro; IPR002138; ICE_p10.			
DR	InterPro; IPR001309; ICE_p20.			
DR	Pfam; PF00655; ICE_p10; 1.			
DR	Pfam; PF00656; ICE_p20; 1.			
DR	PRINTS; PR00376; ILIBCENZYM.			
DR	SMART; SM00115; CASC; 1.			
DR	PROSITE; PS01122; CASPASE_CYS; 1.			
DR	PROSITE; PS01121; CASPASE_HIS; 1.			
DR	PROSITE; PS50207; CASPASE_P10; 1.			
DR	PROSITE; PS50208; CASPASE_P20; 1.			
KM	Protease.			
FT	NON_TER			
SO	SEQUENCE	220 AA;	25050 MW;	FE7F4857CAEBA544 CRC64;
Query Match 20.4%; Score 276; DB 11; Length 220;				
Best Local Similarity 33.3%; Pred. No. 4,8e-15;				
Matches 79; Conservative 39; Mismatches 81; Indels 38; Gaps				
Oy	35	AREGSEVDMEALERNFRYKLFESTMKRDPPTAQQFLDELDFEQOTIDNMEEPSCAFV-VL	93	
Db	6	ARNGDGVDAANLRRTFMGKLYQVRKNDITREDILEMD----	SYSKESHKRSSEFVCYI	61
Oy	94	MAHGEGLLKGDEKMRVLEDLFEVLNNKNCALRCKRPVYIIQAQCRGHRDPGEELRN	153	
Db	62	LSHGEGVYGTNGP-VELKKLTSFPRGDYCSLTGCKPKLFIIOACRGTELDGIE----	116	
Oy	154	BELEGDEELGSEVAVLKNKPNOSIPPTDTLHLYSVESGLSYRHDEKSGFTQTLTD--	211	
Db	117	TDSGDDEEAA-----CQKIPVADPFLVAYSTAPGYSWRNSKQSWFTQSCSL	166	
Oy	212	-VFIIHKSGSLLELTBEITRLMANTENVMOEGK-----PRKNPEVOSTLRKKLY	258	
Db	167	KLYARK----LQPMILTRV--NRKYATPEFSFSDSTFHAKQKPCIVSMLTKEYL	217	
RESULT 5				
ID	Q90BUP7	PRELIMINARY;	PRT;	435 AA.
AC	Q90BUP7;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			

[illegible]

DR EMBL; U77933; AAB96379.1; -.
 DR EMBL; AF136231; AAD3684.1; -.
 DR HSSP; P29466; IICE.
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR002398; ICE.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00655; ICE_p10; 1.
 DR Pfam; PF00656; ICE_p20; 1.
 DR PRINTS; PR00376; I1BCENZYM.
 DR SMART; SM00114; CARD; 1.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS50209; CARD; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 SQ SEQUENCE 452 AA; 50728 MW; 03F9D096BB741CE3 CRC64;

Query Match 20.3%; Score 274.5; DB 11; Length 452;
 Best Local Similarity 30.6%; Pred. No. 1,6e-14;
 Matches 71; Conservative 53; Mismatches 95; Indels 13; Gaps 6;

QY 36 REGSEVDMEALERMFRYLKFESTMKRDPTAQOFLBELDFEQOTIDNMBEPVSCAFVYVMA 95
 Db 219 RSGGDVHTTLVTLFPLGLGYNVHLYDQTAQEWQEKQNFQAQ-LPAHRTVTDSC-IVALLIS 276
 QY 96 HGEELGLGDEKRMVRLFEVLNNKNCALRGKRYVITIQACGEHDPG---ELRLG 152
 Db 277 HGEELGIGVDKLLQLOLVFRLFDNANCPSLQNKPKMFIQACRDEDTDRGVDOODGKN 336
 QY 153 NEELGDEELGDEVAVLKNNPOSIPYTDLHIYSTVEGYLSYRHDEKSGFIQTLTDV 212
 Db 337 HAQSGCGCESDQKXELMK---MRLETRSDMTCGYACLKNAMNRTKXGSMYIEMLTQV 393
 QY 213 FTHKGS--ILELTETIRLMANTEVMOEGK--RKVNPEVQSTLRKKLYL 259
 Db 394 FSEKACDMHVALMVKVNLIKEREQYAGTEFHRCKEMSEYCSLTCQQLYL 445

RESULT 7

Q96AN1 PRELIMINARY; PRT; 277 AA.
 AC Q96AN1;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical 31.6 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LYMPH;
 RA Strausberg R.;
 RL Submitted (NOV-2001) to the EMBL/genbank/DBJ databases.
 DR EMBL; BC016926; AAH16926.1; -.
 DR InterPro; IPR002398; ICE.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR Pfam; PF00655; ICE_p10; 1.
 DR Pfam; PF00656; ICE_p20; 1.
 DR PRINTS; PR00376; I1BCENZYM.
 DR PROSITE; PS01122; CASPASE_CYS; UNKNOWN_1.
 DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 277 AA; 31608 MW; 2F35CD3BC7FF64A CRC64;

Query Match 20.3%; Score 274; DB 4; Length 277;

Best Local Similarity 31.5%; Pred. No. 9.3e-15;
 Matches 86; Conservative 41; Mismatches 104; Indels 42; Gaps 10;
 QY 6 SEMSDPQLQGERRYDMGARLALTLCVTK-----AREGSEVDMEALERMFRYLK 55
 Db 24 SEMSDSGISLDNSYMDYPMGLCIINNKNFHKSTGTTSSGTDVDANLRFTRLNKY 83
 QY 56 ESTMKRDPTAQOFLBELDFEQOTIDNMBEPVSCAFV-VLMAHGEELGLGDEKVMRLD 114
 Db 84 EVRNKNDLTR---BEIELMRDVSKEDHSKRSSFVCLSHGEGILFTNGP-VDLKK 138
 QY 115 LFEVLNNKNCALRGKRYVITIQACGEHDPGEELRGNEELGDEELGGEVAVLKNNP 174
 Db 139 ITNFFRGDRCSRLTGKPKLFIQACRGTLDGIE---TDSQV---DDMACHK--- 186
 QY 175 QSIPTVTDLHIYSTVEGYLSYRHDEKSGFIQTLTDVFIHKKSILELTETIRLMANT 234
 Db 187 --IPEADFLVAYSTAPGYGVRNKSQDSWFIQSIC-AMLQYADKLEFPHMLITRV--NR 241
 QY 235 EYMOEGK-----PRKNPEVQSTLRKKLY 258
 Db 242 KVATFESESFPDPTFAKKQIPCIYVMTLTKELY 274

RESULT 8

Q95NDS PRELIMINARY; PRT; 277 AA.
 AC Q95NDS;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Caspase-3.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxId=9623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21334413; PubMed=11440638;
 RA Muneta Y., Shimotojima Y., Mori Y.;
 RT "Porcine caspase-3: cloning and its activity during apoptosis of
 RT porcine PK15 cells induced by porcine Fas-ligand."
 RL J. Interferon Cytokine Res. 21:409-415(2001).
 DR EMBL; AB029345; BAB5544.1; -.
 DR MEROPS; C14.003; -.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR Pfam; PF00655; ICE_p10; 1.
 DR Pfam; PF00656; ICE_p20; 1.
 DR PROSITE; PS01122; CASPASE_CYS; UNKNOWN_1.
 DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 SQ SEQUENCE 277 AA; 31379 MW; 616C0F56141B012B CRC64;

Query Match 20.2%; Score 273; DB 6; Length 277;
 Best Local Similarity 31.8%; Pred. No. 1.1e-14;
 Matches 83; Conservative 34; Mismatches 100; Indels 44; Gaps 9;

QY 19 YDMGARLALTLCVTK-----AREGSEVDMEALERMFRYLKFESTMKRDPTAQOF 68
 Db 37 YMDYPMGLCIINNKNFDMKATGACRSCTDVAANLRFTRLNKYEVNRKNDLTR-- 93
 QY 69 LEELDFEQOTIDNMBEPVSCAFV-VLMAHGEELGLGDEKVMRLDLEFVLNNKNCAL 127
 Db 94 -BEIELMHSVSKEDHSKRSSFVCLSHGEGKIFGNGP-VDLKLTLSFRRGCCRTL 151
 QY 128 RCKPKYVITIQACGEHDPGEELRGNEELGDEELGDEVAVLKNNPOSIPYTDLHIY 187
 Db 152 TCKPKLFIQACRGTLDGIEITDSCGTE-----DDMAC-----QKIPVADFLVAY 197
 QY 188 STVEGYLSYRHDEKSGFIQTLTDV--FIHKKSILELTETIRLMANTEVMOEG---- 240

Db 198 STAGYVSMRNSKDSWFIQSLCAALKOYVK---LEMLILTRVNRKVAPEFSFSTD 253

Qy 241 ---KPRKVNPEVOSTLRKKLY 258
 Db 254 STFAKKQIPCIIVSMLTRKELY 274

RESULT 9
 Q96KP2 PRELIMINARY; PRT; 277 AA.

AC Q96KP2
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Caspase-3.
 GN CASP3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN RA
 RP Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE FROM N.A.
 RA Oliver L.J.;
 RT "Control of the activation of the procaspase-3 by a sequence located
 RT at the N-terminus of the p17 subunit."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ113269; CAC88866.1; -.
 DR InterPro; IPR002398; ICE.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR Pfam; PF00655; ICE_p10; 1.
 DR Pfam; PF00656; ICE_p20; 1.
 DR PRINTS; PR00376; ILICENZYM.
 DR PROSITE; PS01122; CASPASE_CYS; UNKNOWN_1.
 DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
 DR PROSITE; PSS0207; CASPASE_P10; 1.
 DR PROSITE; PSS0208; CASPASE_P20; 1.
 SQ SEQUENCE 277 AA; 31642 MW; 616276780DD2DE021 CRC64;

Query Match 20.1%; Score 272; DB 4; Length 277;
 Best Local Similarity 31.5%; Pred. No. 1,4e-14;
 Matches 86; Conservative 41; Mismatches 104; Indels 42; Gaps 10;

Qy 6 SEMDPOPLQEE---RYDMSGARLALTLCTK-----AREGSEVDMLEALERFRYLF 55
 Db 24 SEMSDGMSWDTGYKMDYPEWGLCIINNKNFHKSTGWTSGTVDVANLRETFRNLY 83

Qy 56 ESTMKRDPYTAQPFLELDEFOOTIDNWEPRVSCAFV-VLMAGEGGLKGEDEKVRLED 114
 Db 84 EVRKAKNDITR---BEIVELMRDVSKEDHSKRSSFCVLSHGEGGIIFGTNGP-VDLKK 138

Qy 115 LFEVLNNKNCALRGKPKVYIIQACRGEHRDPGEELRGNEELGDEBELGDEVAVLKNNP 174
 Db 139 ITNFFRGRCRSLTGKPKLFIIOACRGTELDGIE---TDSGDV---DDMACHK--- 186

Qy 175 OSIITYDTLTIYSTVEGYLSYRHDKSGFIQTLTDVFIHKKGSILELTEITRLMANT 234
 Db 187 --IIVDADFLVASTAPGYSMRNSKDSWFIQSLC-AMLKQYADKLEFMHILTRV--NR 241

Qy 235 EVMQEGK-----PRKVNPEVOSTLRKKLY 258
 Db 242 KVATEFSFSFDATFPAKKQIPCIIVSMLTRKELY 274

RESULT 10
 Q98UT8 PRELIMINARY; PRT; 282 AA.
 AC Q98UT8
 DT 01-JUN-2001 (Tremblrel. 17, Created)

DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Caspase-3.
 GN CASP3.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN RA
 RP SEQUENCE FROM N.A.
 RA Yabu T., Okazaki T., Yamashita M.;
 RT "Molecular Cloning and Gene Expression of Zebrafish Caspase Related to
 RT Mammalian Caspase-3."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB047003; BAB32409.1; -.
 DR HSP; P42574; 1PAU.
 DR MEROPS; C14.003; -.
 DR ZFIN; ZDB-GENE-011210-1; casp3.
 DR InterPro; IPR002398; ICE.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR Pfam; PF00655; ICE_p10; 1.
 DR Pfam; PF00656; ICE_p20; 1.
 DR PRINTS; PR00376; ILICENZYM.
 DR SMART; SM00115; CASG; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
 DR PROSITE; PSS0207; CASPASE_P10; 1.
 DR PROSITE; PSS0208; CASPASE_P20; 1.
 SQ SEQUENCE 282 AA; 31522 MW; 13C3454F5E09932E CRC64;

Query Match 19.7%; Score 266; DB 13; Length 282;
 Best Local Similarity 29.2%; Pred. No. 4,4e-14;
 Matches 81; Conservative 46; Mismatches 104; Indels 46; Gaps 8;

Qy 9 SDPQPLQEE---RYDMSGARLALTLCTK-----KAREGSEVDMLEALERFRYLF 50
 Db 22 SASQPMQVDAKQSHARYSILNYPNIGHCIINNKNFDRRTGNMFRNGTVDAGNMVNF 81

Qy 51 RYLFESTMKRDPRPAQPFLELDEFOOTIDNWEPRVSCAFV-VLMAGEGGLKGEDEK 108
 Db 82 RKLGYIVKYNVDQFVAIMQVL-----TTVAHDHSCASLVCVLSHGEGVFEGTDT 136

Qy 109 MVRLEDLFEVLNNKNCALRGKPKVYIIQACRGEHRDPGEELRGNEELGDEBELGDEVA 168
 Db 137 -VDIKSLTSLFRGRCRSLTGKPKLFIIOACRGTELDPEVETDHTD-----P 183

Qy 169 VLKNNPQSIPTTYDTLTIYSTVEGYLSYRHDKSGFIQTLTDVFIHKKGSILELTEIT 228
 Db 184 DIPGRERIPVEADFLVASTAPGYSMRNTMTGSWFIQSLCEM-MTKYSELELLQIMT 242

Qy 229 RL-----MANTVMOEGKPRKVNPEVOSTLRKKLY 258
 Db 243 RVNHKVALDEPSTSNMPPFAKKQIPCIIVSMLTRKELY 279

RESULT 11
 Q9ROT0 PRELIMINARY; PRT; 454 AA.
 AC Q9ROT0
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Caspase3.
 GN CASP3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN RA
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20001956; PubMed=10529400;

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DR InterPro: IPR001309; ICE_p20.
DR Pfam: PF00655; ICE_p10; 1.
DR Pfam: PF00656; ICE_p20; 1.
DR PRINTS: PR00376; ILICBNZYME.
DR SMART: SM00115; CASC; 1.
DR PROSITE: PS01122; CASPASE_CYG; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
SQ SEQUENCE 303 AA; 34324 MW; A11728754BF199DD CRC64;

Query Match 19.6%; Score 264.5; DB 11; Length 303;
Best Local Similarity 34.2%; Pred. No. 6,4e-14;
Matches 79; Conservative 35; Mismatches 92; Indels 25; Gaps 8;

OY REGSEVDMDEALERMRYLKFEFTSMKRDPTAOQFLBEDLDFEQOTIDNMEPEVSCAFVTLMA 95
Db 87 RRGDTKDKEALFKFCRSJGFVEVTVNDSCAKM---QDLRRASEDHNSACFACVLLS 143
OY HGESEGLTGDEDEKMWRLDLDLFEVLNNKKCKALKRGPKYVITQACGSEHRDGEELRGNEE 155
Db 144 HGEENLVITGKD-GVTPYIDLTANFRGDRCKTLLKPKLFIQACRGTTLDG----- 194
OY 156 LGGDEELGDEVAVALKNNPO-SIPTVYDTLHISTVEGYLSYRHDEKSGSGFIQTLTDVFI 214
Db 155 IQADSGPIINDTDA----NPKYKIPVEADFLFAYSVPEPYGWSRNGKGSWFQALCSI-L 249
OY 215 HKKGSILELTEBITRL--MANTEVMOEGRKPR---KXNPEVQSTLRKKLY 258
Db 250 NEHGKLEITMQLITRVNDRVARHFEFSQSDPDRFEKKEKQIPCMVSWLTKELY 300

RESULT 13
O9B062 PRELIMINARY; PRT; 416 AA.
AC O9B062;
ID 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 21, Last annotation update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Unknown (protein for WGC:2105) (caspase 9, apoptosis-related cysteine protease
DE (MCH61)).
DE (MCH61).
DE CASP9.
GN CASP9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
OX (1)
RN RP SEQUENCE FROM N.A.
RN RP TISSUE-LNMPH;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RL (2)
RP RP SEQUENCE FROM N.A.
RP RP TISSUE-EYE;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RL (3)
RN RP SEQUENCE FROM N.A.
RA Thomas D.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006463; AAH06463.1; -
DR EMBL; BC002452; AAH02452.1; -
DR EMBL; AL512883; CAC42423.1; -
DR HSSP; P42574; 1PAU.
DR MEROPS: C14.010; -.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00655; ICE_p10; 1.
DR Pfam: PF00656; ICE_p20; 1.

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DR PRINTS, PR00376; ILBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROTEASE.
SQ SEQUENCE 416 AA; 46280 MW; 78E0180DF2A3BD2 CRC64;

Query Match 19.0%; Score 257; DB 4; Length 416;
Best Local Similarity 29.5%; Pred. No. 4e-13;
Matches 75; Conservative 46; Mismatches 89; Indels 44; Gaps 8;

QY 34 KAREGEVDMALERMRYLKFEETMKRDPAAQFLBELDEFOQTINWEEPVSCAFVVL 93
DB 178 RRTGSGNIDCEKLRSSLSHFVMEVKGDLTAKKVLALIELAQDHG--ALDCCVAVI 234
QY 94 MARGEE-----GLKGEDEKVRLEDFEVLNNKCKALRGKPYVYIQACRGEHRDP 146
DB 235 LSHGCGASHLPFGAVVGTGCPVSEKIVNI FNGTSCPSLGKPKLPFIQACGEGQKH 294
QY 147 GBEIRGNEELGDEBELGDEVAVLKNNPQ-----SIPTTDTLHI 186
DB 295 GFEEVASTP--EDESFG-----SNPEPDATPFOGLRTFDQIDAISLPTSDIFVS 344
QY 187 YSTVEGYLSYRHDKSGSFIQTLTDVFIHKKSILELTEETRLMANTVWQEGKPRKN 246
DB 345 YSTFPGVSNRDPKSGSWYETLDDIF--EQMAHSEDLQSLLRVANA-VSKGIYKQM- 400
QY 247 PEVOSTLRKKLYLQ 260
DB 401 PGCFNFKLKKLFFK 414

RESULT 14
Q9JHK1 PRELIMINARY; PRT; 454 AA.
ID 09JHK1
AC 09JHK1;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DE 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Caspase-9 (Caspase-9 long isoform).
GN RNCASP9.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 1)
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Cao G., Chen D., Pei W., O'Horo C., Graham S., Simon R.P., Chen J.;
RT "Cloning and Characterization of Rat Caspase-9: Implication for a Role
RT in Neuronal Cell Death During Brain Development and Transient Cerebral
RT Ischemia.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN
RN
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Itoh T., Itoh A., Pleasure D.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN
RN
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=CEREBELLUM;
RA Cao G., Chen D., Graham S., Simon R.P., Chen J.;
RT "Cloning and Characterization of Rat Caspase-9: Implication for a Role
RT in Neuronal Cell Death During Brain Development and Transient Cerebral
RT Ischemia.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN
RN
RP SEQUENCE FROM N.A.
RC MEDLINE=21192275; PubMed=11278518;
RX

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RA Angelastro J.M., Moon N.Y., Liu D.X., Yang A.-S., Greene L.A.,
RA Franke T.F.;
RT "Characterization of a Novel Caspase-9 Isoform in Rat That Inhibits
RT Apoptosis.";
RL J. Biol. Chem. 276:12190-12200(2001).
RN
RN
RP SEQUENCE FROM N.A.
RC STRAIN=MKY;
RX MEDLINE=21552893; PubMed=11695991;
RA Nishiyama J., Yi X., Venkatesh M.A., Dong Z.;
RT "CDNA cloning and promoter analysis of rat caspase-9.";
RL Biochem. J. 360:49-56(2001).
DR EMBL; AF262319; AAF85658.1; -.
DR EMBL; AF271996; AAF76217.1; -.
DR EMBL; AF286006; AAF99705.1; -.
DR EMBL; AF304659; AAK31519.1; -.
DR EMBL; AY027667; AAK26235.1; -.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.010; -.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00655; ICE_p10; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PRINTS; PR00376; ILBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 454 AA; 50399 MW; 501623B29E6ED6FC CRC64;

Query Match 18.9%; Score 255; DB 11; Length 454;
Best Local Similarity 30.5%; Pred. No. 6.5e-13;
Matches 74; Conservative 49; Mismatches 94; Indels 26; Gaps 8;

QY 36 REGSEVDMALERMFRYLKEESTMKRDPYQAQFLBELDEFOQTIDWKEEVSQAFVYVLA 95
DB 218 RISHVDCEKLRHFCFLRMVAVKNDLTAKKVTALMENAH--RDHRLDCEVVVILS 274
QY 96 HGEE-----GLKGEDEKVRLEDFEVLNNKCKALRGKPYVYIQACRGEHRDPGE 148
DB 275 HGCGASHLPFGAVVGTGCGSVSITERIVNFNGTSCPSLGKPKLPFIQACGEGQKHG 334
QY 149 EL--RGNEBELGDEBELGDEVAVLKNNPQ-----SIPTTDTLHIYSTVEGYLSYR 197
DB 335 EVAFTSQDKAFSDSEPDVPP-VQSGPRTLDDQDANVSSLPITSDILVYSTPFGFVSWR 393
QY 198 HDEKSGCFIOTLTDVFIHKKSILELTEETRLMANTVWQEGKPRKNPEVOSTLRKKL 257
DB 394 DKXSGSWYIETLDDGVL--EQMAHSEDLQSLLRVANA-VSEKGIYKQI-PGCFNFKL 449
QY 258 YLQ 260
DB 450 FPK 452

RESULT 15
Q9IB63 PRELIMINARY; PRT; 399 AA.
ID Q9IB63
AC Q9IB63;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DE 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Caspase-9.
GN XCASPASE-9.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

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OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N. A.
 RX MEDLINE=20209426; PubMed=10744739;
 RA Nakajima K., Takahashi A., Yaita Y.,
 RT "Structure, expression and function of the Xenopus laevis caspase
 RT family";
 RL J. Biol. Chem. 275:10484-10491 (2000).
 DR EMBL; AB038172; BAA94750.1; -.
 DR HSSP; Q15806; 1QDU.
 DR MEROPS; C14.010; -.
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR002398; ICE.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR01309; ICE_p20.
 DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00655; ICE_p10; 1.
 DR Pfam; PF00655; ICE_p20; 1.
 DR PRINTS; PR00376; TLBCENZME.
 DR SMART; SM00114; CARD; 1.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS50209; CARD; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR SEQUENCE 399 AA; 44772 MW; EE2A269719064F9F CRC64;
 SQ

Query Match 18.8%; Score 254; DB 13; Length 399;
 Best Local Similarity 28.0%; Pred. No. 6.6e-13;
 Matches 78; Conservative 42; Mismatches 113; Indels 46; Gaps 9;

QY 15 QEERYDMGARGALATLTVCVT-----KAREGSEVDMLEALRMFRYLKPESTMKRDPT 64
 Db 132 KDKDYPMSDDPIGFLIIINNMNFHECTGLSTRTGSDIDRDKLANMRSPHFVTVKDNLT 191
 QY 65 AQQFLLELDEFQQTIDNMEEPVSCAFVILMANGEE-----GLKGEDEKXVRLLEDLFE 117
 Db 192 GQAM--HDHLQALADODHSLDCCLVILSHGCETRH1QFPGVYGTGDIRIPVERIVS 248
 QY 118 VLNNKNCALRGKPKVYIIQACRGEHRDPGEELRG-----NEELGSD-----ELG 163
 Db 249 YFNGSKCPSLRKPKFI1QACGDDKDKGCEVTSETPLSTSTSLQSDATPVFSGED 308
 QY 164 GDEVAVLKNNPOSIPYTDTLHIYSTVEGYLSYRHDEKSGFIQTLLTDVFIHKGSILEL 223
 Db 309 RDEVDAVSN---IPPSDILVSYSTFPGYVSWRDKHTGSMWVEVLDVLAHHAA---- 360
 QY 224 TBEITRL--MANTEVMOEGKPRKANPEVOSTLRKLYLO 260
 Db 361 -DDLQSLVWVADGVSSKGTYKQI-PGYNPLRKRPYFK 397

Search completed: February 26, 2003, 12:20:28
 Job time : 29.9681 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 26, 2003, 12:14:00 ; Search time 8.19522 Seconds

(without alignments)
1224.772 Million cell updates/sec

Title: US-09-989-903-5

Sequence: 1 MSNPRSLSEERKYMGSALAL.....KARKNPQLQSTLRKRLYLQ 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1234	99.6	242	1	ICEE_HUMAN
2	934.5	75.4	257	1	ICEE_MOUSE
3	305	24.6	424	1	ICED2_CHICK
4	295	23.8	435	1	ICED2_MOUSE
5	289	23.3	435	1	ICED2_HUMAN
6	279.5	22.6	277	1	ICED3_RAT
7	277.5	22.4	277	1	ICED3_CRIO
8	273.5	22.1	277	1	ICED3_MOUSE
9	272.5	22.0	277	1	ICED3_HUMAN
10	270	21.8	303	1	ICED7_MOUSE
11	260	21.0	303	1	ICED7_MOUSE
12	256	20.7	303	1	ICED7_HUMAN
13	248.5	20.1	503	1	ICED3_CAEEL
14	247.5	20.0	339	1	ICED3_MOUSE
15	246.5	19.9	479	1	ICED3_HUMAN
16	245	19.8	496	1	ICED3_MOUSE
17	240.5	19.4	276	1	ICED6_MOUSE
18	237.5	19.2	299	1	ICED1_MOUSE
19	236.5	19.1	404	1	ICED1_MOUSE
20	232.5	18.8	416	1	ICED3_HUMAN
21	227	18.3	282	1	ICED3_HUMAN
22	226.5	18.3	382	1	ICED3_HUMAN
23	225.5	18.2	404	1	ICED3_HUMAN
24	225.5	18.2	323	1	ICED1_MOUSE
25	225	18.0	418	1	ICED3_HUMAN
26	222.5	18.0	386	1	ICED3_HUMAN
27	221.5	17.9	521	1	ICED3_HUMAN
28	218.5	17.6	402	1	ICED3_HUMAN
29	218	17.6	373	1	ICED3_HUMAN
30	217.5	17.6	402	1	ICED3_HUMAN
31	214	17.3	293	1	ICED3_HUMAN
32	213.5	17.2	312	1	ICED3_HUMAN
33	212.5	17.2	405	1	ICED3_HUMAN

34	211	17.0	410	1	ICED3_HUMAN
35	209	16.9	404	1	ICED3_HUMAN
36	205.5	16.6	377	1	ICED3_HUMAN
37	196	15.8	377	1	ICED3_HUMAN
38	193.5	15.6	419	1	ICED3_HUMAN
39	104.5	8.4	484	1	ICED3_HUMAN
40	95.5	7.7	2104	1	ICED3_HUMAN
41	94	7.6	480	1	ICED3_HUMAN
42	91	7.3	510	1	ICED3_HUMAN
43	91	7.3	510	1	ICED3_HUMAN
44	90.5	7.3	520	1	ICED3_HUMAN
45	89.5	7.2	1225	1	ICED3_HUMAN

ALIGNMENTS

RESULT 1
ICED3_HUMAN STANDARD; PRT; 242 AA.
ID ICED3_HUMAN
AC P31944; O95823;
DT 01-JUN-1993 (Rel. 26, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-14 precursor (EC 3.4.22.-) (CASP-14).
GN CASP14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Pover J.-L., Srinivasula S.M., Fernandes-Alnemri T., Alnemri E.S.;
RT "Identification and characterization of human caspase 14.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 68-74; 137-147 AND 154-162.
RC TISSUE=Keratinocytes;
RX MEDLINE=93162043; PubMed=1286667;
RA Raamsen H.H., van Damme J., Puype W., Geeser B., Celis J.E.,
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes.";
RL Electrophoresis 13:960-969 (1992).
CC -!- FUNCTION: MAY BE INVOLVED IN THE DEATH RECEPTOR AND GRANZYME B
CC APOPTOTIC PATHWAYS. MAY FUNCTION AS A DOWNSTREAM SIGNAL TRANSDUCER
CC OF CELL DEATH.
CC -!- SUBUNIT: MAY DIMERIZE WITH LARGE PRODOMAIN CASPASES.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL: AF097874; AAC16173.1;
CC HSP: P29466; IICE.
CC Aarhus/Chent-2PAGE; 6109; IEF.
CC MEROPS; C14.018;
CC Genew; HGNC:1502; CASP14.
CC MIM; 605848;
CC InterPro; IPR002398; ICE.
CC InterPro; IPR002138; ICE_P10.
CC InterPro; IPR001309; ICE_P20.
CC Pfam; PF00655; ICE_P10.1.
CC Pfam; PF00656; ICE_P20.1.
CC PRINTS; PR00376; IICEZYME.
CC SMART; SM00115; CASP; 1.

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DR PROSITE; PS01121; CASPASE_HIS; FALSE_NEG.
DR PROSITE; PS01122; CASPASE_CYS; FALSE_NEG.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolyase; Thiol protease; Apoptosis; Zymogen.
FT PROPEP 1 146 CASPASE-14 SUBUNIT 1 (POTENTIAL).
FT CHAIN ? 146 CASPASE-14 SUBUNIT 2 (POTENTIAL).
FT ACT_SITE 89 242 BY SIMILARITY.
FT ACT_SITE 132 132 BY SIMILARITY.
SQ SEQUENCE 242 AA; 27679 MW; E539FB7EBD908A2 CRC64;

Query Match 99.6%; Score 1234; DB 1; Length 242;
Best Local Similarity 99.6%; Pred. No. 7,8e-93;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRLSEEEKDMSGALALLICTKAREGSEEDLDALHMFRLRFRSTTKRPTAQ 60
DB 1 MSNPRLSEEEKDMSGARLALLICTKAREGSEEDLDALHMFRLRFRSTTKRPTAQ 60
QY 61 FOEELKFOQADSRDPVSCAFVILMAHGRGFLKGDGEMVKLENLFEALNNKCOAL 120
DB 61 FOEELKFOQADSRDPVSCAFVILMAHGRGFLKGDGEMVKLENLFEALNNKCOAL 120
QY 121 RAKPRVYIIQACRGQRDPGETVGGDEIYMWIKDSPQIIPYTDALHYSTVEGYIAYRH 180
DB 121 RAKPRVYIIQACRGQRDPGETVGGDEIYMWIKDSPQIIPYTDALHYSTVEGYIAYRH 180
QY 181 DQKSCFIOTLVDFVTKRKGHILELLETVTRMAEALVQEGKARKTNEIOTSLRKLY 240
DB 181 DQKSCFIOTLVDFVTKRKGHILELLETVTRMAEALVQEGKARKTNEIOTSLRKLY 240
QY 241 LQ 242
DB 241 LQ 242

RESULT 2
ICEE_MOUSE STANDARD; PRT; 257 AA.
ID ICEE_MOUSE
AC 089054;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-14 precursor (EC 3.4.22.-) (CASP-14) (Mm1-ICE) (MICE).
GN CASP14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN 11
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=C57BL/6J; PubMed=9823333;
RX MEDLINE=99040667; PubMed=10203698;
RA Ahmed M., Srinivasula S.M., Hegde R., Mukattash R.,
RA Fernandes-Alnemri T., Alnemri E.S.;
RT "Identification and characterization of murine caspase-14, a new
RT member of the caspase family.";
RL Cancer Res. 58:5201-5205 (1998).
RN 12
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Embryo;
RX MEDLINE=99222069; PubMed=10203698;
RA Van den Craen M., Van Loo G., Pye S., Van Crielinge W.,
RA Vandenbeele P.;
RT "Identification of a new caspase homologue: caspase-14.";
RL Cell Death Differ. 5:838-846 (1998).
RN 13
RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-136.
RX MEDLINE=99009076; PubMed=9792675;
RA Hu S., Snijpae S.J., Vincenz C., Salvesen G., Dixit V.M.;
RT "Caspase-14 is a novel developmentally regulated protease.";

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RL J. Biol. Chem. 273:29648-29653 (1998).
CC -1- FUNCTION: SEEMS TO BE INVOLVED IN THE DEATH RECEPTOR AND GRANZYME
CC B APOPTOTIC PATHWAYS. MAY FUNCTION AS A DOWNSTREAM SIGNAL
CC TRANSDUCER OF CELL DEATH. MAY PLAY A ROLE IN ONTOGENESIS AND SKIN
CC PHYSIOLOGY.
CC -1- SUBUNIT: MAY DIMERIZE WITH LARGE PRODOMAIN CASPASES.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
CC -1- TISSUE SPECIFICITY: EMBRYO, ADULT LIVER AND LESS IN ADULT BRAIN
CC AND KIDNEY.
CC -1- PM: CLEAVAGE BY GRANZYME B, CASPASE-8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC PROTEASE.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -----
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DR EMBL; AF092997; AAC83364.1; -.
DR EMBL; AJ007750; CAA07678.1; -.
DR HSSP; P29466; 1ICE.
DR MEROPS; C14.018; -.
DR MGD; MGI:1335092; Casp14.
DR InterPro; IPR002398; 1ICE.
DR InterPro; IPR002138; 1ICE_P10.
DR InterPro; IPR001309; 1ICE_P20.
DR Pfam; PF00655; 1ICE_P10; 1.
DR Pfam; PF00656; 1ICE_P20; 1.
DR SMART; SMO0115; CASC; 1.
DR PROSITE; PS01121; CASPASE_HIS; FALSE_NEG.
DR PROSITE; PS01122; CASPASE_CYS; FALSE_NEG.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolyase; Thiol protease; Apoptosis; Zymogen.
FT PROPEP 1 7 POTENTIAL.
FT CHAIN 8 257 CASPASE-14 SUBUNIT P18 (POTENTIAL).
FT ACT_SITE 93 93 CASPASE-14 SUBUNIT P11 (POTENTIAL).
FT ACT_SITE 136 136 BY SIMILARITY.
FT MUTAGEN C->A: DECREASE IN DEATH-INDUCING
FT ACTIVITY.
SQ SEQUENCE 257 AA; 29458 MW; A228D88DDBA0EB84 CRC64;

Query Match 75.4%; Score 934.5; DB 1; Length 257;
Best Local Similarity 70.9%; Pred. No. 1.3e-68;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;

QY 1 MSNPRLSEEEKDMSGALALLICTKAREGSEEDLDALHMFRLRFRSTTKRPTAQ 60
DB 5 MSNPRLSEEEKDMSGARLALLICTKAREGSEEDLDALHMFRLRFRSTTKRPTAQ 64
QY 61 FOEELKFOQADSRDPVSCAFVILMAHGRGFLKGDGEMVKLENLFEALNNKCOAL 120
DB 65 FOEELKFOQADSRDPVSCAFVILMAHGRGFLKGDGEMVKLENLFEALNNKCOAL 124
QY 121 RAKPRVYIIQACRGQRDPGETVGGDEIYMWIKDSPQIIPYTDALHYSTVEGYIAYRH 168
DB 125 RAKPRVYIIQACRGQRDPGETVGGDEIYMWIKDSPQIIPYTDALHYSTVEGYIAYRH 183
QY 169 YSTVGYIAYRHQDQSGFIOTLVDFVTKRKGHILELLETVTRMAEALVQEGKARKTN 228
DB 184 YSTVGYIAYRHQDQSGFIOTLVDFVTKRKGHILELLETVTRMAEALVQEGKARKTN 243
QY 229 PEIOTSLRKLYLQ 242
DB 244 PEVOTSLRKLYLQ 257

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RESULT 3
 ID ICE2_CHICK STANDARD; PRT; 424 AA.
 AC 098943;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-1/1S).
 GN CASP2 OR ICH1.
 OS Gallus gallus (chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_Taxid=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White Leghorn; TISSUE=Ovarian granulosa;
 RX MEDLINE=97368127; PubMed=9224894;
 RA Johnson A.L., Bridgham J.T., Bergeron L., Yuan J.;
 RT "Characterization of the avian Ich-1 cDNA and expression of Ich-1L mRNA in the hen ovary";
 RL Gene 192:227-233(1997).
 CC -|- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. MIGHT FUNCTION BY EITHER
 CC ACTIVATING SOME PROTEINS REQUIRED FOR CELL DEATH OR INACTIVATING
 CC PROTEINS NECESSARY FOR CELL SURVIVAL (BY SIMILARITY).
 CC -|- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ICH-1L (SHOWN HERE) AND ICH-1S;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER IN THE N-AND C-
 CC TERMINI. ONLY THE ICH-1L FORM IS FOUND IN THE OVARY.
 CC -|- PTM: HETERODIMER OF A SMALL AND A LARGE SUBUNIT (BY SIMILARITY).
 CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -|- SIMILARITY: CONTAINS 1 CARD DOMAIN.
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 DR EMBL; U64963; AAC29881.1; ALT_INIT.
 DR HSSP; P42574; ICP3.
 DR MEROPS; C14.006; -.
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR002398; ICE.
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR Pfam; PF00619; CARD. 1.
 DR Pfam; PF00655; ICE_P10. 1.
 DR Pfam; PF00656; ICE_P20. 1.
 DR PRINTS; PR00376; TLBCENZTME.
 DR SMART; SM00114; CARD; 1.
 DR SMART; SM00115; CARD; 1.
 DR PROSITE; PS50209; CARD; 1.
 DR PROSITE; PS01122; CASPASE_CYS_1.
 DR PROSITE; PS01121; CASPASE_HIS_1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 KM HydroLase; Thiol protease; Apoptosis; Zymogen; Alternative splicing.
 FT PROPEP 1 140
 FT CHAIN 141 308 CASPASE-2 SUBUNIT P18 (BY SIMILARITY).
 FT CHAIN 309 424 CASPASE-2 SUBUNIT P13 (BY SIMILARITY).
 FT CHAIN 315 424 CASPASE-2 SUBUNIT P12 (BY SIMILARITY).
 FT DOMAIN 7 96 CARD.
 FT ACT_SITE 248 248 BY SIMILARITY.
 FT ACT_SITE 291 291 BY SIMILARITY.
 FT VARSPIC 1 7 MISSING (IN ISOFORM ICH-1S).
 FT VARSPIC 294 424 DETROGDQDCKRSRSPGCEESDANKENLKRLPTPSD
 FT MICGACLKGTAAKRNTRKRSWYIALTYFAEDSRTHVA
 FT DMLVKVRQIKQREGYAGTEFHRCKEMSEYCTLCRDLYL
 FT PPQVPGK -> GVSIGIHILPLPCCHCICCSMRQGEWI

FT REMAKNGQIPQAVRRVWQTRKKISSCVCLHAPI (IN
 FT ISOFORM ICH-1S).
 SQ SEQUENCE 424 AA; 47959 MW; 792810508B8B2F60 CRC64;
 Query Match 24.6%; Score 305; DB 1; Length 424;
 Best Local Similarity 31.5%; Pred. No. 1.9e-17;
 Matches 86; Conservative 51; Mismatches 82; Indels 54; Gaps 10;
 QY 1 MSNRSLEEEKYDMSGALALILC-----VTKAREGSEEDIDALEHMFROUPESTM 52
 DB 166 ISEPR-----GLALLISNHFSSSEKDELYSGGDVDCASLEFLKHLGYQTV 213
 QY 53 KRDPFAQFOEELKFOQALDSREDPVSCAFVLMAGREGFLKGDGEMVYLENLFEAL 112
 DB 214 FHDQSAEEMSGALERFSKLPD-HQDVDS-C-IVALLSHVEGVGTQDKLLQLQEARFLF 271
 QY 113 NKKGQALRAKPKYITIOACRGEDPDG-ETVGDDELVMYIKDSP-----Q 157
 DB 272 DNANCPMLQNKPKMFFIQACGDETDGVDQDSKE---RSDSPGCEESDANKENLKL 327
 QY 158 TIPTYDALHYSTVEGVYAVRHQDKSCFIOTLVDFTK--RKHILLETVEYTRMAE 215
 DB 328 RLPTPSDWICGYACKGTAAKRNTRKRSWYIALTYFAEDSRTHVADMLVKVRQIKQ 387
 QY 216 AEIVQEGKARKTN-----PEIQSTLRKRLYL 241
 DB 388 ---REGYAPGTEFHRCKEMSEYCTLCRDLYL 416
 RESULT 4
 ID ICE2_MOUSE STANDARD; PRT; 435 AA.
 AC P29594; O08737;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (NEDD2
 DE protein).
 GN CASP2 OR ICH1 OR NEDD2 OR NEDD2-2.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c.
 RX MEDLINE=95047319; PubMed=7958843;
 RA Kumar S., Kinoshita M., Noda M., Copeland N.G., Jenkins N.A.;
 RT "Induction of apoptosis by the mouse Nedd2 gene, which encodes a
 RT protein similar to the product of the *Caenorhabditis elegans* cell
 RT death gene *ced-3* and the mammalian IL-1 beta-converting enzyme.";
 RL Genes Dev. 8:1613-1626(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/An;
 RX MEDLINE=97190206; PubMed=9038361;
 RA van de Graen M., Vandenabeele P., Declercq W., van den Brande I.,
 RA van Loo G., Molemans F., Schotte P., van Cielinge W., Beyaert R.,
 RA Fiers W.;
 RT "Characterization of seven murine caspase family members";
 RL FEBS Lett. 403:61-69(1997).
 RN [3]
 RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92328780; PubMed=1378265;
 RA Kumar S., Tomooka Y., Noda M.;
 RT "Identification of a set of genes with developmentally down-regulated
 RT expression in the mouse brain.";
 RL Biochem. Biophys. Res. Commun. 185:1155-1161(1992).
 CC -|- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. MIGHT FUNCTION BY EITHER
 CC ACTIVATING SOME PROTEINS REQUIRED FOR CELL DEATH OR INACTIVATING
 CC PROTEINS NECESSARY FOR CELL SURVIVAL. MAY BE IMPORTANT IN

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CC MULTISTEP CARCINOGENESIS.
CC -1- SUBUNIT: HETERODIMER OF A SMALL AND A LARGE SUBUNIT (BY
CC SIMILARITY).
CC -1- TISSUE SPECIFICITY: HIGH LEVEL EXPRESSION SEEN IN THE EMBRYONIC
CC CNS, LIVER, LUNG, KIDNEY, SMALL INTESTINE, AND HAIR FOLLICLES OF
CC VIBRISAE. MODERATE EXPRESSION SEEN IN THE SKIN, ORAL MUCOSA,
CC SKELETAL MUSCLE, SUBMANDIBULAR GLAND AND THYMUS. IN THE ADULT, IT
CC IS HIGHLY EXPRESSED IN SPLEEN, LUNG AND KIDNEY. MODERATELY IN THE
CC BRAIN, HEART, TESTIS, LIVER. LOW LEVELS IN THE THYMUS, SKELETAL
CC MUSCLE, OVARY AND GUT.
CC -1- DEVELOPMENTAL STAGE: DURING EMBRYONIC DEVELOPMENT IS HIGHLY
CC EXPRESSED IN SEVERAL TYPES OF MOUSE TISSUE UNDERGOING HIGH RATES
CC OF PROGRAMMED CELL DEATH SUCH AS CENTRAL NERVOUS SYSTEM AND
CC KIDNEY.
CC -1- PFM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
CC THAT OF OTHER CASPASES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -----
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CC -----
CC EMBL; D28492; BA25876.1; ALT_INIT.
CC EMBL; Y13085; CA473527.1; ALT_INIT.
CC HSSP; P42574; ICP3.
CC MEROPS; C14.006; -.
CC MGD; MGI:97295; Casp2.
CC InterPro; IPR001315; CARD.
CC InterPro; IPR002398; ICE.
CC InterPro; IPR002138; ICE_p10.
CC InterPro; IPR001309; ICE_p20.
CC Pfam; PF00619; CARD; 1.
CC Pfam; PF00655; ICE_p10; 1.
CC Pfam; PF00656; ICE_p20; 1.
CC PRINTS; PR00376; IILBENZYM.
CC SMART; SM00114; CARD; 1.
CC SMART; SM00115; CASC; 1.
CC PROSITE; PS50209; CARD; 1.
CC PROSITE; PS01122; CASPASE_CYS; 1.
CC PROSITE; PS01121; CASPASE_HIS; 1.
CC PROSITE; PS0207; CASPASE_P10; 1.
CC PROSITE; PS0208; CASPASE_P20; 1.
CC Hydrolase; Thiol protease; Apoptosis; Zymogen.
CC K1M PROPEP 1 152
CC FT CHAIN 153 316 CASPASE-2 SUBUNIT P18 (BY SIMILARITY).
CC FT CHAIN 317 435 CASPASE-2 SUBUNIT P13 (BY SIMILARITY).
CC FT CHAIN 331 435 CASPASE-2 SUBUNIT P12 (BY SIMILARITY).
CC FT DOMAIN 15 103 CARD.
CC FT ACT_SITE 260 260 BY SIMILARITY.
CC FT ACT_SITE 303 303 BY SIMILARITY.
CC FT MUTAGEN 303 303 C->G: LOSS OF FUNCTION.
CC FT CONFLICT 71 71 MISSING (IN REF. 1).
CC SQ SEQUENCE 435 AA; 48896 MW; 8984E6AA7E7676 CRC64;

Query Match 23.8%; Score 295; DB 1; Length 435;
Best Local Similarity 31.5%; Pred. No. 1.2e-16;
Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

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Db 320 HTSPGCEESDAGKEELMKR-----LPTSRDMIQVACLKGNAAMRNTKGSWYIEALT 374
Oy 193 DVETKR--KGHLELTTEVTRMAEALVQEGKAKTN-----PEIQSTLRKRLYL 241
Db 375 QVFSERACDMHVDMLVKNALIKE---RGVAPGTFHFKCKMSEYICSTLCOOLYL 428

RESULT 5
ID ICE2_HUMAN STANDARD; PRT; 435 AA.
AC P42575; P42576;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-
DE 11/15).
GN CASP2 OR ICH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=94373811; PubMed=8087842;
RT Wang L., Miura M., Bergeron L., Zhu H., Yuan J.;
RT "Ich-1, an Ice/ced-3-related gene, encodes both positive and negative
RT regulators of programmed cell death.";
RT Cell 78:739-750(1994).
RN [2]
RP CLEAVAGE SITES.
RX MEDLINE=96206041; PubMed=8654923;
RA Xue D., Shahan S., Horvitz H.R.;
RT "The Caenorhabditis elegans cell death protein CED-3 is a cysteine
RT protease with substrate specificities similar to those of the human
RT Cpp32 protease.";
RL Genes Dev. 10:1073-1083(1996).
CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. MIGHT FUNCTION BY EITHER
CC ACTIVATING SOME PROTEINS REQUIRED FOR CELL DEATH OR INACTIVATING
CC PROTEINS NECESSARY FOR CELL SURVIVAL.
CC -1- SUBUNIT: HETERODIMER OF A SMALL AND A LARGE SUBUNIT (BY
CC SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ICH-1L (SHOWN HERE) AND ICH-1S;
CC ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER IN THE N-AND C-
CC TERMINI. ICH-1L ACTS AS A POSITIVE REGULATOR OF APOPTOSIS, WHEREAS
CC ICH-1S FUNCTIONS AS A NEGATIVE REGULATOR OF APOPTOSIS.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LARGER AMOUNTS IN THE EMBRYONIC
CC LUNG, LIVER AND KIDNEY THAN IN THE HEART AND BRAIN. IN THE ADULTS
CC HIGHER LEVEL EXPRESSION IS SEEN IN THE PLACENTA, LUNG, KIDNEY,
CC PANCREAS THAN IN THE HEART, BRAIN, LIVER AND SKELETAL MUSCLE.
CC -1- PFM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
CC THAT OF OTHER CASPASES.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -----
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CC -----
CC EMBL; U13021; AA58959.1; -.
CC EMBL; U13022; AA58960.1; -.
CC HSSP; P29466; IICE.
CC MEROPS; C14.006; -.
CC Genew; HGNC:1503; CASP2.
CC MIM; 600639; -.
CC InterPro; IPR001315; CARD.
CC InterPro; IPR002398; ICE.
CC InterPro; IPR002138; ICE_p10.

```

DR InterPro: IPR001309; ICE_p20.
 DR Pfam: PF00619; CARD; 1.
 DR Pfam: PF00655; ICE_p10; 1.
 DR Pfam: PF00656; ICE_p20; 1.
 DR PRINTS: PR00376; ILIBCNZYME.
 DR SMART: SM00114; CARD; 1.
 DR SMART: SM00115; CASC; 1.
 DR PROSITE: PS50209; CARD; 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 DR HydroLase: Thiol protease; Apoptosis; Zymogen; Alternative splicing.
 KW PROPEP 1 152
 FT CHAIN 153 308 CASPASE-2 SUBUNIT P18.
 FT PROPEP 309 316
 FT CHAIN 317 435 CASPASE-2 SUBUNIT P13.
 FT CHAIN 331 435 CASPASE-2 SUBUNIT P12.
 FT DOMAIN 15 103 CARD.
 FT ACT_SITE 260 260 BY SIMILARITY.
 FT ACT_SITE 303 303 BY SIMILARITY.
 FT VARSPIC 1 14 MISSING (IN ISOFORM ICH-1S).
 FT VARSPIC 306 435 DETROGVDQDQGNKHAASPGCESDAGEKLPKRLPTRSD
 MTCGACLCGTAANKTKGWSYEAIAQVFSERACDMHYA
 DMLVKNVALIKDRGVAGTEFHRCKEMSEYCSLCHRLYL
 FPGHPT -> GGAIGSLGHLLFTATASIAL (IN
 ISOFORM ICH-1S).
 FT MUTAGEN 303 303 C-S: LOSS OF FUNCTION.
 FT MUTAGEN 352 352 A->T: LOSS OF FUNCTION.
 SQ SEQUENCE 435 AA; 4885 MW; 1652EC7JF6286F87 CRC64;
 Query Match 23.3%; Score 289; DB 1; Length 435;
 Best Local Similarity 31.1%; Pred. No. 3.8e-16;
 Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;
 QY 29 REGSEEDIDALEHMFROJFESTMKRDPJTAQFOEELKFOQDAISREDPVSCAFVILMA 88
 DB 202 RSGGDVHSTLVTLFKLGVVHVLCDDTAQBMOKLQNFQO-LPAHRTDSC-IVALLS 259
 QY 89 HGRSGFLKGESEVWVKNLELFEALNKNKCALBAKPKYIIIOACRGEDRG----- 140
 DB 260 HGVGALITGVGKLLQLOEVLPFNANCPSLQNKPKMFLOACGDDTDGVDQDQGN 319
 QY 141 -----ETVGDSEIWWIVKIDSPOTTIPTYDALHVSVEGYIAYRHDKGSCFIQTLV 192
 DB 320 HAGSPGESDAGE-----KLPRKRLPTRSDMTCGACLCGTAANKTKGWSYTELA 374
 QY 193 DVFTKR--KGHILELLEVTTRMAEALIVGSGKARKN-----PEIQSTLRKRLYL 241
 DB 375 QVFSEACDMHVDMLVKNVALIKD---REGVAGTEFHRCKEMSEYCSLCHRLYL 428
 RESULT 6
 ICES_RAT STANDARD; PRT; 277 AA.
 ID ICES3_RAT
 AC P55213; P70543; Q62993; P97699;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
 protein) (CPP-32) (Caspase-3) (SREBP cleavage activity 1)
 DE (SCA-1) (LICE) (IRP).
 GN CASP3 OR CPP32.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eultheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96358624; PubMed=8761296;
 RA Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
 RA Fletcher F.A.;
 RT "Molecular characterization of mouse and rat CPP32 beta gene encoding

RT a cysteine protease resembling interleukin-1 beta converting enzyme
 RT and CED-3.";
 RL Oncogene 13:749-755 (1996).
 RN [2]
 RP SEQUENCE OF 30-241 FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=96042508; PubMed=7588240;
 RA Flaws J.A., Kugu K., Trbovich A.M., Desanti A., Tilly K.I.,
 RA Hirschfield A.N., Tilly J.L.;
 RT "Interleukin-1 beta-converting enzyme-related proteases (IRPs) and
 RT mammalian cell death: dissociation of IRP-induced oligonucleosomal
 RT endonuclease activity from morphological apoptosis in granulosa cells
 RT of the ovarian follicle.";
 RL Endocrinology 136:5042-5053 (1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97184204; PubMed=9030616;
 RA Ni B., Wu X., Du Y., Su Y., Hamilton-Byrd E., Rockey P.K.,
 RA Rostek P. Jr., Poirier G.G., Paul S.M.;
 RT "Cloning and expression of a rat brain interleukin-1beta-converting
 RT enzyme (ICE)-related protease (IRP) and its possible role in
 RT apoptosis of cultured cerebellar granule neurons.";
 RL J. Neurosci. 17:1561-1569 (1997).
 RN [4]
 RP SEQUENCE OF 1-264 FROM N.A.
 RA Yakovlev A.G.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT
 CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
 CC 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROID REGULATORY
 CC ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-
 CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
 CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).
 CC -1- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, LIVER, AND MUSCLE
 CC BUT NOT IN KIDNEY OR TESTIS.
 CC -1- DEVELOPMENTAL STAGE: HIGHLY EXPRESSED IN NEURON-ENRICHED REGIONS
 CC OF THE DEVELOPING BRAIN, BUT DOWN-REGULATED TO LOW LEVELS IN THE
 CC ADULT BRAIN.
 CC -1- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -----
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 CC -----
 CC EMBL: U49930; AAC52765.1; -
 CC EMBL: U34685; AAC52261.1; -
 CC EMBL: U84410; AAB41792.1; -
 CC EMBL: U58656; AAB02722.1; -
 CC HSSP: P42574; 1PAU.
 CC MEROPS: C14.003; -
 DR InterPro: IPR002398; ICE.
 DR InterPro: IPR002138; ICE_p10.
 DR InterPro: IPR001309; ICE_p20.
 DR Pfam: PF00655; ICE_p10; 1.
 DR Pfam: PF00656; ICE_p20; 1.
 DR PRINTS: PR00376; ILIBCNZYME.
 DR SMART: SM00115; CASC; 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.

DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 KW Hydrolyase; Thiol protease; Zymogen; Apoptosis.
 FT PROPEP 1 9
 FT PROPEP 10 28 BY SIMILARITY.
 FT CHAIN 29 175 APOPAIN P17 SUBUNIT.
 FT ACT_SITE 121 121 APOPAIN P12 SUBUNIT.
 FT ACT_SITE 163 163 BY SIMILARITY.
 FT CONFLICT 25 29 KSMDS -> QVD (IN REF. 4).
 FT CONFLICT 170 170 C -> S (IN REF. 2).
 FT CONFLICT 178 178 T -> A (IN REF. 2).
 FT CONFLICT 182 182 M -> V (IN REF. 2).
 FT CONFLICT 187 187 I -> K (IN REF. 2).
 FT CONFLICT 190 190 E -> G (IN REF. 3).
 FT CONFLICT 199 199 T -> S (IN REF. 2).
 FT CONFLICT 211 211 D -> G (IN REF. 2).
 FT CONFLICT 236 236 L -> I (IN REF. 4).
 FT CONFLICT 245 245 T -> M (IN REF. 3).
 SQ SEQUENCE 277 AA; 31491 MW; ADABFA18E2507402 CRC64;

Query Match 22.6%; Score 279.5; DB 1; Length 277;
 Best Local Similarity 32.8%; Pred. No. 1.3e-15;
 Matches 82; Conservative 35; Mismatches 106; Indels 27; Gaps 8;

QY 9 BEKYMSGALALILCVT-----KARGSEEDLDALHMFROLFESTMKRDPYA 58
 DB 34 DSYAMDPEMKLCITINKNKPHKSTGMSARKGTVDANLAFETMALKYEVRRNKDILTR 93
 QY 59 EGFQSELEKFOQAIIDREDPVSCAFVLMAGREGFLKGEDEMYKLENLFEALNNKQ 118
 DB 94 BEIMELMDSVSKEDHSKRSSFVC--VILSHGDEGVIFGTNGP-VDLKCLTSFFRGDYCR 149
 QY 119 ALRAKPKYIIQACGEQRPDGE-ETVSGDEITVMVKDSQITPTTDAHYVSTEGYIA 177
 DB 150 SLTGPKPKFIIOACRGTELDGCIETDSGTDDMAC---QKIPVADFLYAVSTAPGYYS 205
 QY 178 YHDDKSGSCFIOTLVDFYFKRGHILE--LLEVTYRMA---EAEVQEGKARKTNP 230
 DB 206 WNSNDGWFIOISLC-AMKLVAHKLFEFMHILTRVNRKVAATEPESFLDATPAKQIDPC 264
 QY 231 IOSTLRKRLY 240
 DB 265 IYVSLTKELY 274

RESULT 7
 ICE3_CRILLO STANDARD; PRT; 277 AA.
 ID ICE3_CRILLO
 AC 060431;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE APOPAIN precursor (BC 3.4.22.-) (Cysteine protease CPP32) (Yama
 DE protein) (CPP-32) (caspase-3) (CASP-3) (SREBP cleavage activity 1)
 DE (SCA-1).
 GN CASP3 OR CPP32.
 OS Cricetus longicaudatus (long-tailed hamster) (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 OC NCBI_TaxID=10030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RC MEDLINE=96183185; PubMed=8605870;
 RA Wang X., Zelenek N.G., Yang J., Sakai J., Brown M.S.,
 RA Goldstein J.L.;
 RT "Cleavage of sterol regulatory element binding proteins (SREBPs) by
 RT CPP32 during apoptosis";
 RT EMBL J. 15:1012-1020(1996).
 RL
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES

CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT
 CC PROTOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
 CC 216-ASP-GLY-217 BOND. CLEAVES AND ACTIVATES STEROID REGULATORY
 CC ELEMENT BINDING PROTEINS (SREBPs) BETWEEN THE BASIC HELIX-LOOP-
 CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
 CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).
 CC SUBUNIT: HETERODIMER OF A 17 KDA (P17) AND A 12 KDA (P12) SUBUNIT
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- PTM: CLEAVAGE BY GRANTZYME B, CASPASE-6, -8 AND -10 GENERATES THE
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 CC CASPASE-7. PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.

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 CC -----
 CC EMBL; U27463; AAB01511.1; -.
 DR HSSP; P42574; 1PAU.
 DR MEROPS; C14.003; -.
 DR InterPro; IPR002398; ICE.
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR Pfam; PF00655; ICE_P10; 1.
 DR Pfam; PF00656; ICE_P20; 1.
 DR PRINTS; PR00376; ILIACENZYM.

DR SMART; SMO0115; CASC; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 KW Hydrolyase; Thiol protease; Zymogen; Apoptosis.
 FT PROPEP 1 9
 FT PROPEP 10 28 BY SIMILARITY.
 FT CHAIN 29 175 APOPAIN P17 SUBUNIT.
 FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
 FT ACT_SITE 121 121 BY SIMILARITY.
 FT ACT_SITE 163 163 BY SIMILARITY.
 SQ SEQUENCE 277 AA; 31612 MW; 0BF3A4590A2828A3 CRC64;

Query Match 22.4%; Score 277.5; DB 1; Length 277;
 Best Local Similarity 35.9%; Pred. No. 1.8e-15;
 Matches 79; Conservative 31; Mismatches 93; Indels 17; Gaps 7;

QY 29 REGSEEDLDALHMFROLFESTMKRDPYAFQFQSELEKFOQAIIDREDPVSCAFVLM 88
 DB 64 RSGTVDAAKRETFMALKYEVRRNKDILREIVELMNASDEHSKRSSFVC--VILS 120
 QY 89 HREGSEFLKGEDEMYKLENLFEALNNKQALRAKPKYIIQACGEQRPDGE-ETVSGDE 147
 DB 121 HDDEVITGTDP-IDLKCLTSYFRGDCYRSLIKRKFIIIOACRGTELDGCIETDSGTE 179
 QY 148 IVMVTKDSPQITPTTDAHYVSTEGYIAVRHDDKSGCFIOTLVDFYFKRGHILE-- 204
 DB 180 DDMTC---QKIPVADFLYAVSTAPGYYSNRNPNPDGSGWFIOSLSMW-KLVAKLEFMH 234
 QY 205 LLEVTYRMA---EAEVQEGKARKTNPETOSTLRKRLY 240
 DB 235 ILTRVNRKVAATEPESFLDSTPAKQIDPCIVSMLTKELY 274

RESULT 8
 ICE3_MOUSE STANDARD; PRT; 277 AA.
 ID ICE3_MOUSE
 AC P70677; O08668;

SEQUENCE FROM N.A. (ALPHA AND BETA ISOFORMS).
 RC TISSUE=T-cell;
 RX MEDLINE=95074098; PubMed=7983002;
 RA "Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
 RT "CPP32, a novel human apoptotic protein with homology to
 RT "Caothababitis elegans cell death protein Ced-3 and mammalian
 RT interleukin-1 beta-converting enzyme.";
 RL J. Biol. Chem. 269:30761-30764 (1994).
 RN [12]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95292347; PubMed=7774019;
 RA "Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
 RA "Beidler D.R., Poirier G.G., Salvesen G.S., Dixit V.M.;
 RT "Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable
 RT protease that cleaves the death substrate poly(ADP-ribose)
 RT polymerase.";
 RL Cell 81:801-809 (1995).
 RN [13]
 RP SEQUENCE OF 29-46 AND 175-193, AND FUNCTION.
 RX MEDLINE=95319529; PubMed=7596430;
 RA Nicholson D.W., Ali A., Thornberry N.A., Vailancourt J.P., Ding C.K.,
 RA Gallant M., Gareau Y., Griffin P.R., Labelle M., Lazebnik V.A.,
 RA Munday N.A., Raju S.M., Smolton M.E., Yamin T.-T., Li V.L.,
 RA Miller D.K.;
 RT "Identification and inhibition of the ICE/CED-3 protease necessary
 RT for mammalian apoptosis.";
 RL Nature 376:37-43 (1995).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 28-277.
 RX MEDLINE=96266352; PubMed=8673606;
 RA Rocanda J., Nicholson D.W., Fazil K.M., Gallant M., Gareau Y.,
 RA Labelle M., Peterson E.P., Rasper D.M., Ruel R., Vailancourt J.P.,
 RA Thornberry N.A., Becker J.W.;
 RT "The three-dimensional structure of apopain/CPP32, a key mediator of
 RT apoptosis.";
 RL Nat. Struct. Biol. 3:619-625 (1996).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.
 RX MEDLINE=97197830; PubMed=9045680;
 RA Mitel P.R., di Marco S., Krebs J.F., Bai X., Karanewsky D.S.,
 RA Priestle J.P., Tomaselli K.J., Grutter M.G.;
 RT "Structure of recombinant human CPP32 in complex with the
 RT tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone.";
 RL J. Biol. Chem. 272:6539-6547 (1997).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE=20283632; PubMed=10821855;
 RA Lee D., Long S.A., Adams J.L., Chan G., Vaidya K.S., Francis T.A.,
 RA Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S.,
 RA Levy M.A., Demolfi W.E. Jr., Keller P.M., Tomaszek T., Head M.S.,
 RA Ryan M.D., Haltiwanger R.C., Liang P.-H., Janson C.A., McDevitt P.J.,
 RA Johanson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,
 RA Lark M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E.;
 RT "Potent and selective nonpeptide inhibitors of caspases 3 and 7
 RT inhibit apoptosis and maintain cell functionality.";
 RL J. Biol. Chem. 275:16007-16014 (2000).
 RN [17]
 RP PROCESSING.
 RX MEDLINE=9635383; PubMed=8755496;
 RA "Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
 RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
 RA Litwack G., Alnemri E.S.;
 RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
 RT apoptotic cysteine protease containing two FADD-like domains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469 (1996).
 RN [18]
 RP CLEAVAGE OF HUNTINGTIN.
 RX MEDLINE=96331285; PubMed=8696339;
 RA Goldberg Y.P., Nicholson D.W., Rasper D.M., Kalchman M.A., Koide H.B.,
 RA Graham R.K., Brown M., Kazemi-Esfarjani P., Thornberry N.A.,
 RA Vailancourt J.P., Hayden M.R.;
 RT "Cleavage of huntingtin by apopain, a procaspotic cysteine protease,
 RT is modulated by the polyglutamine tract.";

Nat. Genet. 13:442-449 (1996).
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT
 CC PROTOLOGICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
 CC 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROID REGULATORY
 CC ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-
 CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
 CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9. INVOLVED IN THE
 CC CLEAVAGE OF HUNTINGTIN.
 CC -1- ENZYME REGULATION: INHIBITED BY ISATIN SULFONAMIDES.
 CC -1- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SPLEEN, HEART, LIVER
 CC AND KIDNEY. MODERATE LEVELS IN BRAIN AND SKELETAL MUSCLE, AND LOW
 CC IN TESTIS. ALSO FOUND IN MANY CELL LINES, HIGHEST EXPRESSION IN
 CC CELLS OF THE IMMUNE SYSTEM.
 CC -1- PTM: CLEAVAGE BY GRANTSYME B, APAF-1, CASPASE-6, -8 AND -10
 CC GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE
 CC PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE
 CC ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT
 CC OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
 CC AND VICE VERSA.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -----
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL: U13737; AAA65015.1; -
 CC EMBL: U13738; AAB60355.1; -
 CC EMBL: U26943; AAA74929.1; -
 CC PDB: 1PAU; 07-JUL-97.
 CC PDB: 1CP3; 24-DEC-97.
 CC PDB: 1GFW; 23-JUN-00.
 CC MEROPS: C14.003; -
 CC GeneID: HGNC:1504; CASP3.
 CC MIM: 600636; -
 CC InterPro: IPR002398; ICE.
 CC InterPro: IPR001384; ICE_P10.
 CC InterPro: IPR001309; ICE_P20.
 CC Pfam: PF00655; ICE_P10; 1.
 CC Pfam: PF00656; ICE_P20; 1.
 CC PRINTS: PR00376; TLBCENZME.
 CC SMART: SM00115; CASc; 1.
 CC PROSITE: PS01122; CASPASE_CYS; 1.
 CC PROSITE: PS01121; CASPASE_HIS; 1.
 CC PROSITE: PS50207; CASPASE_P10; 1.
 CC PROSITE: PS50208; CASPASE_P20; 1.
 CC HydroLase; Thiol protease; Zymogen; Apoptosis; Polymorphism;
 KW 3D-structure.
 FT PROPEP 1 9
 FT PROPEP 10 28
 FT CHAIN 17 175 APOPAIN P17 SUBUNIT.
 FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
 FT ACT_SITE 121 121 BY SIMILARITY.
 FT ACT_SITE 163 163 BY SIMILARITY.
 FT VARIANT 190 190 D -> E (IN ISOFORM BETA).
 FT /FTID=VAR_001401.
 SQ SEQUENCE 277 AA; 31594 MW; 8634DD2ACE6EF64B CRC64;
 Query Match 22.0%; Score 272.5; DB 1; Length 277;
 Best Local Similarity 31.9%; Pred. No. 4.6e-15;
 Matches 80; Conservative 39; Mismatches 103; Indels 29; Gaps 9;
 QY 9 EEKYMGAALALILICVKK-----ARSGSEDDALEHMFPROLPFSTMRDPTA 58
 DB 34 DNSTKMDPPEMLCIIINNNKPHKSTGTSRSCTVDVDAANLRETRNLKYEVNRKNDLRL 93
 QY 59 EGFQEELEKFOAIDSRDPVSCAFVLMAGRGEGFLKGEDG--EMVKLENLEFALNNKN 116


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Db 94 BEIYELMRDVSKEHSHKSSKSFVC---VLLSHGEGIIFGTNGPVDLKKITNF---RGDR 147
Oy 117 COALRAKPVYIIQACRGEGRDPG-ETVGSDEIYVWIKDSQTIPTYDALHYVSTEGY 175
Db 148 CRSLTGRPKFTIIOACKRTETDCCGETDSGVDDMAC---HKIPVADFLYAVSTARGY 203
Oy 176 IAYHDDKSGSCFIOTLVDFVFTK--RKGHILELLEVTFRMA-EAEIVQ---EGKARKTP 229
Db 204 YSMNNSDGSFIIOSLCMLKQYADKLEPHMILTRVNRKVKATFEFSFDFATFPAKQIP 263
Oy 230 EIOSTLRKRLY 240
Db 264 CIVSMILTKELY 274

RESULT 10
ID ICE7_MOUSE STANDARD; PRT; 303 AA.
AC P97864; 008669;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (LICE2 cysteine protease) (apoptotic
DE protease Mch-3).
GN CASP7 OR MCH3 OR LICE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=97224489; Pubmed=9070923;
RA Juan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Fletcher F.A.;
RT "Identification and mapping of Casp7, a cysteine protease resembling
RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3.";
RL Genomics 40:86-93(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97236307; Pubmed=9125129;
RA Mukasa T., Khoroku Y., Tsukahara T., Momoi M.Y., Kimura I.,
RA Momoi T.;
RT "Mortmainin enhances CPP32-like activity during neuronal
RT differentiation of P19 embryonal carcinoma cells induced by retinoic
RT acid.";
RL Biochem. Biophys. Res. Commun. 232:192-197(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; Pubmed=9038361;
RA van de Craen M., Vandenabeele P., Declercq W., van den Brande I.,
RA van Ioo G., Molemans F., Schotte P., van Crielinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).
RN [4]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL
CC REGULATORY ELEMENT BINDING PROTEINS (SREBPS). OVEREXPRESSION
CC PROMOTES PROGRAMMED CELL DEATH (BY SIMILARITY).
CC -!- SUBUNIT: HETERODIMER OF A 20 kDa (p20) AND A 11 kDa (p11) SUBUNIT.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, LUNG, LIVER, AND
CC KIDNEY. LOW LEVELS IN SPLEEN, SKELETAL MUSCLE, AND TESTIS. NO
CC EXPRESSION IN THE BRAIN.
CC -!- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF

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CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U67321; AAC53068.1; ALT_INIT.
DR EMBL; D66353; BAA19730.1; -.
DR EMBL; Y13088; CAA73530.1; -.
DR EMBL; BC005428; AAH05428.1; -.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.004; -.
DR MGD; MGI:109383; Casp7.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR Pfam; PF00655; ICE_P10; 1.
DR Pfam; PF00656; ICE_P20; 1.
DR PRINTS; PR00376; IL1BCENZME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR KX Hydrolyase; Thiol protease; Zymogen; Apoptosis.
DR PROPEP 1 23 BY SIMILARITY.
FT CHAIN 24 198 CASPASE-7 SUBUNIT P20 (BY SIMILARITY).
FT PROPEP 199 206 BY SIMILARITY.
FT CHAIN 207 303 CASPASE-7 SUBUNIT P11 (BY SIMILARITY).
FT ACT SITE 144 144 BY SIMILARITY.
FT ACT SITE 186 186 BY SIMILARITY.
FT CONFLICT 10 11 EL -> DW (IN REF. 2).
FT CONFLICT 45 45 A -> T (IN REF. 2).
FT CONFLICT 48 49 VR -> RQ (IN REF. 2).
SQ SEQUENCE 303 AA; 34060 MW; 747787B5BDE5F744 CRC64;

Query Match 21.8%; Score 270; DB 1; Length 303;
Best Local Similarity 32.6%; Pred. No. 8,3e-15;
Matches 71; Conservative 36; Mismatches 101; Indels 10; Gaps 4;

Oy 29 REGSEEDLALAHNFRLRFESTWKRDPDPAEQELEKFOQALDSREDPVSCAFVVLMA 88
Db 87 RNGTHDKDAGALFKCFQVILGFEVTHNDCSCAKMDDLKRSASEEDHSNS---ACFACVLLS 143
Oy 89 HGRGFLKGEDEGVKLENFEALNNKQCALRAKPVYIIQACRGEGRDPGRTVSGDEI 148
Db 144 HGEEDLLYGGDG-VTPKIDLTANFRGRCKTLEKPLFTIQACRGTELDGIGQADSGPI 202
Oy 149 VMVYKDSQPTIPTYTDALHYVSTEGYIAYRHDDKSGSCFIOTLVDFVFTK--RKGHILEL 206
Db 203 NDIANPRNKIPVADFLPAYSTVPGYVSWNRNPKGSGWPFQALCSILNENKDELEIQIL 262
Oy 207 TEVTRMAEAEIVQEGAR---KTNEIQTLRKRLY 240
Db 263 TRVNDVRAHPSGSDPFRNEKQIPCMVSMILTKELY 300

RESULT 11
ID ICE7_MESAU STANDARD; PRT; 303 AA.
AC P55214;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (ICE-1-like apoptotic protease 3)
DE (ICE-LAP3) (Apoptotic protease Mch-3) (SREBP cleavage activity 2)
DE (SCA-2).

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GN CASP7 OR MCH3.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=Syrian; TISSUE=Liver;
 RX MEDLINE=96224303; PubMed=8643593;
 RA Pal U.-T., Brown W.S., Goldstein J.L.;
 RT "Purification and cDNA cloning of a second apoptosis-related cysteine
 RT protease that cleaves and activates sterol regulatory element binding
 RT proteins";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:5437-5442(1996).
 CC
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL
 CC REGULATORY ELEMENT BINDING PROTEINS (SREBPs). PROTEOLYTICALLY
 CC CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-|-GLY-217
 CC BOND. OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH (BY
 CC SIMILARITY).
 CC
 CC -1- SUBUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT
 CC (BY SIMILARITY).
 CC
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC
 CC -1- PTM: CLEAVAGES BY GRANTZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
 CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
 CC CPP32. PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).
 CC
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC
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 CC
 CC -----
 CC EMBL: U47332; AAC52595.1; -
 CC HSSP: P42574; IPAU.
 CC
 CC DR MEROPS: C14.004; -
 CC DR InterPro: IPR002398; ICE.
 CC DR InterPro: IPR002138; ICE_P10.
 CC DR InterPro: IPR001309; ICE_P20.
 CC
 CC DR Pfam: PF00655; ICE_P10; 1.
 CC DR Pfam: PF00656; ICE_P20; 1.
 CC DR PRINTS: PR00376; ILHCENZYM.
 CC DR SMART: SM00115; CASC; 1.
 CC
 CC DR PROSITE: PS01122; CASPASE_CYS; 1.
 CC DR PROSITE: PS01121; CASPASE_HIS; 1.
 CC DR PROSITE: PS50207; CASPASE_P10; 1.
 CC DR PROSITE: PS50208; CASPASE_P20; 1.
 CC
 CC KW Hydrolase; Thiol protease; Zymogen; Apoptosis.
 CC
 CC FT CHAIN 1 23
 CC FT CHAIN 24 198 CASPASE-7 SUBUNIT P20.
 CC FT PROPEP 199 206 BY SIMILARITY.
 CC FT CHAIN 207 303 CASPASE-7 SUBUNIT P11.
 CC FT ACT_SITE 144 144 BY SIMILARITY.
 CC FT ACT_SITE 186 186 BY SIMILARITY.
 CC SQ SEQUENCE 303 AA; 34037 MW; EA29356D90984648 CRC64;

Query Match 21.0%; Score 260; DB 1; Length 303;
 Best Local Similarity 31.7%; Pred. No. 5.3e-14;
 Matches 69; Conservative 39; Mismatches 100; Indels 10; Gaps 5;

QY 29 REGSEEDLALHEMFQRLPFEFTMKRDPFAEQFQELKFOQAIDSRDPVSCAFVYVMA 88
 DB 87 RKTGTDADALPFCFSLGFDVVVYVNDSCAKKQDILRKASDEPHNS---ACFACVLIS 143
 QY 89 HGRGEGFLKSGEGMVKLENIFFALNNKNCQALAKPKRYVYIIQACRGQRDPGFTVGDEI 148
 DB 144 HGBENLIYKMGD-VTPIDKILTAHFRGDRCKTLLKPKLFTIQACRGTELDGDVGQADSGPI 202

QY 149 VMVIXDSPQITPTVTDALHYSTVEGYIAYRHDKGSCFIQTLVDVETK--RKGHILELL 206
 DB 203 NETDANRKYKIPVADFLPAVSTVPGYVSWRNPKGSMFQALCSIDHKGKLEIMQIL 262
 QY 207 TEVTRRNA--EAEVDE-GKARTNPEIOSTLRKLY 240
 DB 263 TRVNDRAVHRFESOCDDPCFNEKKOIPCMVSMLTKEYL 300
 RESULT 12
 ID C77_HUMAN STANDARD; PRT; 303 AA.
 AC P55210; Q13364; Q96BA0;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Caspase-7 precursor (BC 3.4.22.-) (ICE-like apoptotic protease 3)
 DE (ICE-LAP3) (Apoptotic protease Mch-3) (CWH-1).
 GN CASP7 OR MCH3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 OK
 RN [1]
 RP SEQUENCE FROM N.A. (ALPHA ISOFORM).
 RX MEDLINE=96139498; PubMed=8576161;
 RA Duan H., Chinnaiyan A.M., Hudson P.L., Wing J.P., He W.-W.,
 RA Dixit V.M.;
 RT "ICE-LAP3, a novel mammalian homologue of the Caenorhabditis elegans
 RT cell death protein Ced-3, is activated during Fas- and tumor necrosis
 RT factor-induced apoptosis";
 RL J. Biol. Chem. 271:1621-1625(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ALPHA ISOFORM).
 RC TISSUE=Spleen;
 RX MEDLINE=96147144; PubMed=8567622;
 RA Lipke J.A., Gu Y., Sarnacki C., Caron P.R., Su M.S.-S.;
 RT "Identification and characterization of CPP32/Mch2 homolog 1, a novel
 RT cysteine protease similar to CPP32";
 RL J. Biol. Chem. 271:1825-1828(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ALPHA AND BETA ISOFORMS).
 RC TISSUE=T-cell;
 RX MEDLINE=96105019; PubMed=8521391;
 RA Fernandes-Alnemri T., Takahashi A., Armstrong R.C., Krebs J.,
 RA Fritz L.C., Tomaselli K.J., Wang L., Xu Z., Croce C.M., Salvenson G.,
 RA Earnshaw W.C., Litwack G., Alnemri E.S.;
 RT "Mch3, a novel human apoptotic cysteine protease highly related to
 RT CPP32";
 RL Cancer Res. 55:6045-6052(1995).
 RN [4]
 RP SEQUENCE FROM N.A. (ALPHA AND ALPHA' ISOFORMS).
 RC TISSUE=Fetal lung, and Fetal spleen;
 RX MEDLINE=97224489; PubMed=9070923;
 RA Juan T.S.-C., McViee I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
 RA Copeland N.G., Fletcher F.A.;
 RT "Identification and mapping of Casp7, a cysteine protease resembling
 RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3";
 RL Genomics 40:86-93(1997).
 RN [5]
 RP SEQUENCE FROM N.A. (ALPHA ISOFORM).
 RC TISSUE=Skin;
 RA Strauberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP PROCESSING.
 RX MEDLINE=9635838; PubMed=8755496;
 RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
 RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
 RA Litwack G., Alnemri E.S.;
 RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
 RT apoptotic cysteine protease containing two FAD-like domains";

RL	Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).	
CC	- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL	
CC	REGULATORY ELEMENT BINDING PROTEINS (SREBPs). PROTEOLYTICALLY	
CC	CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP- -GLY-217	
CC	BOND. OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH.	
CC	- ENZYME REGULATION: INHIBITED BY ISATIN SUBNAMIDES.	
CC	- SUBUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT.	
CC	- SUBCELLULAR LOCATION: Cytoplasmic.	
CC	- ALTERNATIVE PRODUCTS: 3 ISOFORMS; ALPHA (SHOWN HERE), BETA AND	
CC	ALPHA'; ARE PRODUCED BY ALTERNATIVE SPLICING. THE BETA ISOFORM IS	
CC	NOT PROTEOLYTICALLY ACTIVE.	
CC	- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SKELETAL MUSCLE,	
CC	LIVER, KIDNEY, SPLEEN AND HEART, AND MODERATELY IN TESTIS. NO	
CC	EXPRESSION IN THE BRAIN.	
CC	- PWM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE	
CC	SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY	
CC	CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF	
CC	CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND	
CC	VICE VERSA.	
CC	- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.	
CC	- CAUTION: WHAT WE CALL ALPHA' ISOFORM IS KNOWN IN REF. 4 AS BETA,	
CC	BUT AS BETA IS ALREADY DEFINED IN REF. 3 WE HAVE CALLED IT ALPHA'.	
CC	-----	
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CC	or send an email to license@isb-sdb.ch).	
CC	-----	
DR	EMBL; U39613; AAC50346.1; -	
DR	EMBL; U40281; AAC50352.1; -	
DR	EMBL; U37448; AAC50303.1; -	
DR	EMBL; U37449; AAC50304.1; -	
DR	EMBL; U67319; AAC51152.1; -	
DR	EMBL; U67320; AAC51153.1; -	
DR	EMBL; U67206; AAF21460.1; -	
DR	EMBL; BC015799; AAH15799.1; -	
DR	HSSP: P42574; 1PAU.	
DR	MEROPS: C14.004; -	
DR	Genew; HGNC:1508; CASP7.	
DR	MIM; 601761; -	
DR	InterPro; IPR002398; ICE.	
DR	InterPro; IPR002138; ICE_p10.	
DR	InterPro; IPR001309; ICE_p20.	
DR	Pfam; PF00655; ICE_p10; 1.	
DR	Pfam; PF00656; ICE_p20; 1.	
DR	PRINTS; PR00376; IL1BCENZYM.	
DR	SMART; SMO0115; CASC; 1.	
DR	PROSITE; PS01122; CASPASE_CYS; 1.	
DR	PROSITE; PS01121; CASPASE_HIS; 1.	
DR	PROSITE; PS0207; CASPASE_P10; 1.	
DR	PROSITE; PS50208; CASPASE_P20; 1.	
KW	Hydrolase; Thiol protease; Zymogen; Apoptosis; Alternative splicing.	
FT	PROPEP	1 23
FT	CHAIN	198
FT	PROPEP	199 206
FT	CHAIN	207 303
FT	ACT_SITE	144 144
FT	ACT_SITE	186 186
FT	VASPLIC	1 1
FT	VASPLIC	149 303
FT	M -> MDCGMPGRKMKHLEKNTSCGGSSGICASYVTQM	
FT	(IN ISOFORM ALPHA').	
FT	EUIDDGIQADSGINIDTANPRKRIEVDADFVASTVGGY	
FT	SWRSRGSGWFWQALCSILIEHGKDLIEIMQITRVNDVAR	
FT	HFEESQDPHFPEKKQICPCVSMLTRELYFSQ -> MESCS	
FT	VTOAGVQRDILGRLOPPRLAEGSLIMWASPTGPGSMTO	
FT	MILDTRSQMKLTSSPTLRPAITRGAGQAEAPGLCASP	
FT	PSMRSTETKWSCKRSPG (IN ISOFORM BETA).	
FT	C->A: NO APOPTOTIC ACTIVITY.	
FT	D -> E (IN REF. 5).	
FT	CONFLICT 4 4	

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FT CONFLICT 194 194 G -A (IN REF. 1).
SQ SEQUENCE 303 AA; 34276 MW; CD373EB54A232CA4 CRC64;
Query Match 20.7%; Score 256; DB 1; Length 303;
Best Local Similarity 30.7%; Pred. No. 1,1e-13;
Matches 67; Conservative 39; Mismatches 102; Indels 10; Gaps 4;

OY 29 REGSEEDLDALAHMFPROLPFESTYMKRDPTAOFQOELEKFOQALDSREDPVYSCAFVILMA 88
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 143
DB 87 RRGCTKDADALFKPCFRSGFDVIVVNDSCAKMODLLKK---ASEEDHTNACFACILLIS 143
OY 89 HOREDFLAGEGGEWMLKLNLFALNNKKCOALRAKPKYIIIOACRGGEORDGETYGGDEI 148
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 202
DB 144 HGEENVIVYIGKDG-VPIPKDLTAHFGRDCKTKLLEPKXLFYIACRGYELDDGIGQADSGPI 202
OY 149 VWVIVDSQGTPTTYDALAHVSTVEGYIAYRHDDKQSCFCFIOTLVDFVFK--RKGHILEL 206
DB 203 NDTDANPPYKPIPEVDFLFANSTVGYISMSPRGSGFVVALCSILEHKGDELEIMQIL 262
OY 207 TEVTRRMAEALVQEG---KARKTNPETIOSTLRKRLY 240
DB |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 263
DB 263 TRVNDRVARHFESQSDDPHFHEKQIPCVVSMILTKELY 300

RESULT 13
CED3_CAEEL STANDARD; PRT; 503 AA.
AC P42573; P45435; O9NMQ8;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cell death protein 3 precursor (EC 3.4.22.-).
GN CED-3 OR C48D1.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilita; Rhabditoidea;
OC Rhabdilitae; Pelodetinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A. AND MUTAGENESIS.
RC STRAIN=Bristol N2;
RX MEDLINE=94061982; PubMed=8242740.
RA Yuan J., Shaham S., Ledoux S., Ellis H.M., Horvitz H.R.;
RT "The C. elegans cell death gene ced-3 encodes a protein similar to
RT mammalian interleukin-1 beta-converting enzyme.";
RL Cell 75:641-652(1993).
RN [2]
RP REVISION TO 418.
RA Horvitz H.R.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Burton J.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP REVISIONS.
RA Durbin R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ACTS AS A CYSTEINE PROTEASE IN CONTROLLING PROGRAMMED
CC CELL DEATH BY PROTOPLASMICALLY ACTIVATING OR INACTIVATING A
CC SUBSTATE PROTEIN OR PROTEIN, A POTENTIAL INHIBITOR MAY BE CED-4.
CC ALTERNATIVELY IT MIGHT DIRECTLY CAUSE CELL DEATH BY
CC PROTOPLASMICALLY CLEAVING PROTEINS THAT ARE CRUCIAL FOR CELL
CC VIABILITY.
CC -1- SUBUNIT: COULD BE A HETERODIMER OF TWO SUBUNITS DERIVED FROM THE
CC PRECURSOR SEQUENCE BY A PROBABLE AUTOCATALYTIC MECHANISM.
CC -1- DEVELOPMENTAL STAGE: MOST ABUNDANT DURING EMBRYOGENESIS AND IS
CC ALSO DETECTED AT LATER STAGES.
CC -1- PTM: MAY BE REGULATED BY PHOSPHORYLATION.
CC -1- SIMILARITY: BELONGS TO PERTIDASE FAMILY C14.
CC -1- SIMILARITY: CONTAINS 1 CAD DOMAIN.
CC -----
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DR EMBL; L29052; AAA27982.2; -
 DR EMBL; AP210702; AAG42045.1; -
 DR EMBL; Z81049; CAB61001.2; -
 DR WormPep; C48D1.2; CE29088.
 DR HSSP; P42574; ICP3.
 DR MEROPS; C14.002; -
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR003398; ICE.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00655; ICE_p10; 1.
 DR Pfam; PF00656; ICE_p20; 1.
 DR PRINTS; PR00376; ILBCENZME.
 DR SMART; SM00114; CARD; 1.
 DR SMART; SM00115; CARD; 1.
 DR PROSITE; PS50209; CARD; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR HydroLase; Thiol protease; Apoptosis, Phosphorylation.
 KW CHAIN 1 371
 FT CHAIN 372 503
 FT CHAIN 372 503
 FT DOMAIN 1 91
 FT ACT_SITE 107 205
 FT ACT_SITE 304 304
 FT ACT_SITE 358 358
 FT MUTAGEN 27 27
 FT MUTAGEN 65 65
 FT MUTAGEN 360 360
 FT MUTAGEN 449 449
 FT MUTAGEN 466 466
 FT MUTAGEN 483 483
 FT MUTAGEN 486 486
 SQ SEQUENCE 503 AA; 56616 MW; 722D5831F94DA69 CnC64;

Query Match 20.1%; Score 248.5; DB 1; Length 503;
 Best Local Similarity 27.9%; Pred. No. 8.5e-13;
 Matches 68; Conservative 42; Mismatches 93; Indels 41; Gaps 6;

QY 29 REGSEDDALAHMFRQLRFESTMKRDPRAEQFQELKFOQAIDSRREDPVCAPVUMA 88
 DB 259 RRGTRADKKNLNLPRCMGYVICKNLGRGMLLTIRDFAR---HESHGSAIILVLS 314
 QY 89 HOREGFLKGEDEMYLLELFEALNNKNCQALRAKPKVYIIQACGEQRPGETV----- 143
 DB 315 HGEENVITGVDDIPSTHETIYDLNNAANPRLANKKXIFVQACRERDNGFPVLDSVD 374
 QY 144 -----GGEDEVVYKSP-----QTIPYTDALHAYSTVEGIAYR 179
 DB 375 GVPAFLRRGMDN-----RDGPLFNFPLGCVRPQVQVWRKKPSQADILILVYATTAQVSWR 429
 QY 180 HQKSGCFIOTLVDT--KRKHITELLTEYTRMAAEALVQEG-KAKTNPETIOSTR 236
 DB 430 NSARGSWFIQAVCEVSTHAKMDVLETVNKKVACGFGTSQGSNLIKQPEMTSRLL 489
 QY 237 KRLY 240
 DB 490 KKFY 493

RESULT 14
 ICE_DROME

ID ICE_DROME STANDARD; PRT; 339 AA.
 AC 001382; Q9VAH1;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Caspase precursor (EC 3.4.22.-) (drtice).
 GN ICE OR CG7788.
 OS Drosophila melanogaster (fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP TISSUE=Embryo;
 RX MEDLINE=97327558; PubMed=9184225;
 RA Fraser A.G., Evan G.I.,
 RT "Identification of a Drosophila melanogaster ICE/CED-3-related
 RT protease, drice.";
 RL EMBO J. 16:2805-2813(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-U., Andrews-Plamkoch C., Baldwin D.,
 RA Ballwey R.M., Baeu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Boltschakov S.,
 RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman I.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalish J., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodedge T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -!- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. ACTS DOWNSTREAM OF RPR.
 CC CLEAVES BACULOVIRUS P35 AND LAMIN DMO IN VITRO.
 CC -!- SUBUNIT: HETERODIMER OF A 21 KDa (P21) AND A 12 KDa (P12) SUBUNIT.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED AT ALL STAGES WHERE APOPTOSIS
 CC OCCURS.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -----
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DR EMBL: Y12261; CA72937.1; -
 DR EMBL: AE003771; AAF56939.1; -
 DR HSSP: P42574; IPAU.
 DR MEROPS: C14.015; -
 DR FLYBASE: FBgn0019972; Ice.
 DR InterPro: IPR002398; ICE.
 DR InterPro: IPR002138; ICE_P10.
 DR InterPro: IPR001309; ICE_P20.
 DR Pfam: PF00655; ICE_P10; 1.
 DR Pfam: PF00656; ICE_P20; 1.
 DR PRINTS: PR00376; ILICENZYME.
 DR SMART: SM00115; CASc; 1.
 DR PROSITE: PS01122; CASPASE_Cys; 1.
 DR PROSITE: PS01121; CASPASE_His; 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 KM Hydrolyase; Thiol protease; Zymogen; Apoptosis.
 FT PROPP 1 28 BY SIMILARITY.
 FT CHAIN 29 217 CASPASE SUBUNIT P21 (BY SIMILARITY).
 FT PROPP 218 230 BY SIMILARITY.
 FT CHAIN 231 339 CASPASE SUBUNIT P12 (BY SIMILARITY).
 FT ACT SITE 169 169 BY SIMILARITY.
 FT ACT SITE 211 211 BY SIMILARITY.
 FT CONFLICT 151 151 A -> S (IN REF. 1).
 FT CONFLICT 265 265 S -> T (IN REF. 1).
 FT SEQUENCE 339 AA; 37363 MW; E105ED29518507EC CRC64;

Query Match 20.0%; Score 247.5; DB 1; Length 339;
 Best Local Similarity 30.5%; Pred. No. 6,3e-13;
 Matches 60; Conservative 42; Mismatches 76; Indels 19; Gaps 5;

QY 27 KAREGEEDLDALHEMRQRLFEESTMKRDPFAEQFOEELKFGQALDSREDPVSQAFVL 86
 DB 110 KSRAGTIVDCENLTVRLVKQDLFEVTYVDC--RYKDLRTIEVAASQNHSDSCILVAI 166
 QY 87 MAHGREFLKGEDEWVKTLELFEALNNKNGQALRAKPKVYIIQACGEQDPETV--- 143
 DB 167 LSHGEWYIYAKDTQ-YKLDNWSFPTANHCPSLAGRKLFIDACQCDRLDGGVTMORS 225
 QY 144 ----GGDEIVWVINDSPQITPTYTDALHVSVEGYIAYRHDKGSCFIOTLVVFTK-- 197
 DB 226 QTEVDG-----SSMSYKIPVHADFLIAYISTVDFGFSMRTTSGSMFQSLCAELANG 279
 QY 198 RKGHLELLEVTERRMA 214
 DB 280 KRDLITLLTFVCCORVA 296

RESULT 15
 ICE8_HUMAN STANDARD; PRT; 479 AA.
 ID ICE8_HUMAN STANDARD; PRT; 479 AA.
 AC Q14750; Q14791; Q14792; Q14793; Q14794; Q14795; Q14796; Q15780;
 AC Q15806; Q9U081; Q14676;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Caspase-8 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 5)
 DE (MORT1-associated CED-3 homolog) (MACH) (FADD-homologous ICE/CED-3-
 DE like protease) (FADD-like ICE) (FLICE) (Apoptotic cysteine protease)
 DE (Apoptotic protease Mch-5) (CASP4).
 GN CASP8 OR MCH5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Thymus, and B-cell;

RX MEDLINE=96279826; PubMed=8681376;
 RA Boldin M.P., Goncharov T.M., Goltsev Y.V., Wallach D.,
 RT "Involvement of MACH, a novel MORT1/FADD-interacting protease, in
 RT Fas/APO-1- and TNF receptor-induced cell death";
 RL Cell 85:803-815(1996).
 RN [12]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=96279827; PubMed=8681377;
 RA Muzio M., Chinaiyan A.M., Kischkel F.C., O'Rourke K., Shevchenko A.,
 RA Ni J., Scaffidi C., Bretz J.D., Zhang M., Gentz R., Mann M.,
 RA Krammer P.H., Peter M.E., Dixit V.M.;
 RT "FLICE, a novel FADD-homologous ICE/CED-3-like protease, is recruited
 RT to the CD95 (Fas/APO-1) death-inducing signaling complex";
 RL Cell 85:817-827(1996).
 RN [13]
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE=96353838; PubMed=8755496;
 RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
 RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
 RA Litwack G., Alnemri E.S.;
 RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
 RT apoptotic cysteine protease containing two FADD-like domains";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
 RN [14]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99132295; PubMed=9931493;
 RA Grenet J., Teitz T., Wei T., Valentine V., Kidd V.J.;
 RT "Structure and chromosome localization of the human CASP8 gene";
 RL Gene 226:225-232(1999).
 RN [15]
 RP SEQUENCE FROM N.A. (ISOFORM 2-ALPHA).
 RX MEDLINE=97373543; PubMed=9228018;
 RA Srinivasula S.M., Ahmed M., Oltie S., Bullrich F., Banks S.,
 RA Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J.,
 RA Armstrong R.C., Alnemri E.S.;
 RT "FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates
 RT Fas/TNFR1-induced apoptosis";
 RL J. Biol. Chem. 272:18542-18545(1997).
 RN [16]
 RP PARTIAL SEQUENCE, AND PROCESSING.
 RX MEDLINE=97121412; PubMed=8962078;
 RA Srinivasula S.M., Ahmed M., Fernandes-Alnemri T., Litwack G.,
 RA Alnemri E.S.;
 RT "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1
 RT protease Mch5 is a CrmA-inhibitable protease that activates multiple
 RT Ced-3/ICE-like cysteine proteases";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).
 RN [17]
 RP FUNCTION.
 RX MEDLINE=97160607; PubMed=9006941;
 RA Muzio M., Salvesen G.S., Dixit V.M.;
 RT "FLICE induced apoptosis in a cell-free system. Cleavage of caspase
 RT zymogens";
 RL J. Biol. Chem. 272:2952-2956(1997).
 RN [18]
 RP PROCESSING.
 RX MEDLINE=97327557; PubMed=9184224;
 RA Medema J.P., Scaffidi C., Kischkel F.C., Shevchenko A., Mann M.,
 RA Krammer P.H., Peter M.E.;
 RT "FLICE is activated by association with the CD95 death-inducing
 RT signaling complex (DISC)";
 RL EMBO J. 16:2794-2804(1997).
 RN [19]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE=99451259; PubMed=10508784;
 RA Blanchard H., Kodandapani L., Mitali P.R.E., Di Marco S., Krebs J.F.,
 RA Wu J.C., Tomaselli K.J., Gruttler M.G.;
 RT "The three-dimensional structure of caspase-8: an initiator enzyme in
 RT apoptosis";
 RL Structure 7:1125-1133(1999).
 CC -!- FUNCTION: MOST UPSTREAM PROTEASE OF THE ACTIVATION CASCADE OF
 CC CASPASES RESPONSIBLE FOR THE FAS-RECEPTOR MEDIATED (CD95) AND

CC TNFR-1 INDUCED CELL DEATH: BINDING TO THE ADAPTOR MOLECULE FADD
 CC RECRUITS IT TO EITHER RECEPTORS. THE RESULTING AGGREGATE CALLED
 CC THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS FLICE/MACH
 CC PROTEOLYTIC ACTIVATION. THE ACTIVE DIMERIC ENZYME IS THEN
 CC LIBERATED FROM THE DISC AND FREE TO ACTIVATE DOWNSTREAM APOPTOTIC
 CC PROTEASES. PROTEOLYTIC FRAGMENTS OF THE N-TERMINAL PROPEPTIDE
 CC (TERMED CAP3, CAP5 AND CAP6) ARE LIKELY RETAINED IN THE DISC.
 CC CLEAVAGES AND ACTIVATES CASPASE-3, -4, -6, -7, -9, AND -10. MAY
 CC PARTICIPATE IN THE GRANZYME B APOPTOTIC PATHWAYS. PROTEOLYTICALLY
 CC CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP). HYDROLYZES THE SMALL-
 CC MOLECULE SUBSTRATE, AC-ASP-GLU-VAL-ASP-|-AMC. LIKELY TARGET FOR
 CC THE COMPLEX VIRUS CRMA DEATH INHIBITORY PROTEIN.
 CC SUBUNIT: HETERODIMER OF A 18 kDa (P18) AND A 10 kDa (P10) SUBUNIT.
 CC INTERACTS WITH CFLAR.
 CC -1- ALTERNATIVE PRODUCTS: 8 ISOFORMS; 1-ALPHA (SHOWN HERE), 2-
 CC ALPHA/MCH5-BETA, 3-ALPHA, 4-ALPHA, 1-BETA, 2-BETA, 3-BETA AND 4-
 CC BETA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ALPHA 1 AND BETA 1 ISOFORMS ARE EXPRESSED IN A
 CC WIDE VARIETY OF TISSUES. HIGHEST EXPRESSION IN PERIPHERAL BLOOD
 CC LEUKOCYTES, SPLEEN, THYMUS, AND LIVER. BARELY DETECTABLE IN BRAIN,
 CC TESTIS, AND SKELETAL MUSCLE.
 CC -1- PM: GENERATION OF THE SUBUNITs REQUIRES ASSOCIATION WITH THE
 CC DISC, WHEREAS ADDITIONAL PROCESSING IS LIKELY DUE TO THE
 CC AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. GRANZYME B AND
 CC CASPASE-10 CAN BE INVOLVED IN THESE PROCESSING EVENTS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -1- SIMILARITY: CONTAINS 2 DEATH EFFECTOR DOMAINS (DED).
 CC -----
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 CC -----
 CC EMBL; X98172; CAA66853.1; -
 CC EMBL; X98173; CAA66854.1; -
 CC EMBL; X98174; CAA66855.1; -
 CC EMBL; X98175; CAA66856.1; -
 CC EMBL; X98176; CAA66857.1; -
 CC EMBL; X98177; CAA66858.1; -
 CC EMBL; X98178; CAA66859.1; -
 CC EMBL; U58143; AAC50602.1; -
 CC EMBL; U60520; AAC50645.1; -
 CC EMBL; AF102146; AAD24962.1; -
 CC EMBL; AF102139; AAD24962.1; JOINED.
 CC EMBL; AF102140; AAD24962.1; JOINED.
 CC EMBL; AF102141; AAD24962.1; JOINED.
 CC EMBL; AF102142; AAD24962.1; JOINED.
 CC EMBL; AF102143; AAD24962.1; JOINED.
 CC EMBL; AF102144; AAD24962.1; JOINED.
 CC EMBL; AF102145; AAD24962.1; JOINED.
 CC EMBL; AF009620; AAB70913.1; -
 CC PDB; 1ODU; 10-JUL-00.
 CC MEROPS; C14.009; -
 CC GeneW; HGNC:1509; CASP8.
 CC MIM; 601763; -
 CC InterPro; IPR001875; DED.
 CC InterPro; IPR002138; ICE_P10.
 CC InterPro; IPR001309; ICE_P20.
 CC Pfam; PF00655; ICE_P10; 1.
 CC Pfam; PF00656; ICE_P20; 1.
 CC Pfam; PF01335; DED; 2.
 CC PROSITE; PS01122; CASPASE_CYS; 1.
 CC PROSITE; PS01121; CASPASE_HIS; 1.
 CC PROSITE; PS50207; CASPASE_P10; 1.
 CC PROSITE; PS50208; CASPASE_P20; 1.
 CC PROSITE; PS50168; DED; 2.
 CC Hydrolase; Thiol peptidase; Apoptosis; Zymogen; Alternative splicing;
 CC Repeat; 3d-structure.
 CC PROPEP 1 216
 CC CHAIN 217 374 CASPASE-8 SUBUNIT P18.

FT PROPEP 375 384
 FT CHAIN 385 479
 FT ACT_SITE 317 317
 FT ACT_SITE 360 360
 FT DOMAIN 2 80
 FT DOMAIN 100 177
 FT VARSPPLIC 102 102
 FT VARSPPLIC 184 198
 FT VARSPPLIC 184 220
 FT VARSPPLIC 184 267
 FT VARSPPLIC 199 235
 FT VARSPPLIC 221 479
 FT VARSPPLIC 236 479
 FT VARSPPLIC 269 276
 FT VARSPPLIC 277 479
 FT CONFLICT 285 285
 FT CONFLICT 294 294
 FT CONFLICT 331 331
 FT SEQUENCE 479 AA; 55391 MW; 7A5FEADA6B39B582F CRC64;
 SQ
 Query Match 19.9%; Score 246.5; DB 1; Length 479;
 Best Local Similarity 29.7%; Pred. No. 1.2e-12;
 Matches 80; Conservative 37; Mismatches 115; Indels 37; Gaps 9;

QY 3 NPRSLSEERK-----YDMSCAALALILCV-----TKARE-----GSEEDLDAL 39
 DB 211 SPREDSSQTLDKYQKSKRGVCLINNHPAKAREKPKXLSINDRNGTHDAQAL 270
 QY 40 EHMFRQLRPESTMKRDPFAEQFOEELKFOQALDSREDPVSCAFVLMAGREGFLKED 99
 DB 271 TTFPELHFIEIKPHDDCTVEQIYEILKIYQLMDHSHNM-----CFICCLISHGDKGIYGTD 327
 QY 100 GEMVLENTLFEALNNKNCQALRAKPKYIIOACRGEQCDPEVTGSD-----IYVWINDS 155
 DB 328 GQEADIVELTSGFTGLKCPSLAGKPKVFPIQACQGDNYQKGIPIVETDSEEOPIYLMDS 387
 QY 156 POT--IPTYTDAHVYSTVEGYIAYRHQKSGSCFIQTLVDVFTKR--XG-HILELLTEVT 210
 DB 368 POTRIIPDEADPDLGMAIVNNCVSYRNPAGETWYQSLQSLRRCRPGDDILTLTEVN 447
 QY 211 RMAEAEIVQEGKARKKTNPEIQSTLRKRL 239
 DB 448 YEVSND--DKKMGKQMPQPTFLRKRL 474

Search completed: February 26, 2003, 12:19:26
 Job time : 9.19522 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 26, 2003, 12:20:36 ; Search time 9.64143 Seconds
(without alignments)
946.818 Million cell updates/sec

Title: US-09-989-903-5
Perfect score: 1239
Sequence: 1 MSNPRSLSEEEKYDMSGALAL.....KARKTNPETQSTURKRLYLQ 242

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174566 seqs, 37721826 residues

Total number of hits satisfying chosen parameters: 174566

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/2/pubppaa/PTCT_NEW_PUB pep.*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB pep.*
4: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB pep.*
5: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB pep.*
6: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB pep.*
7: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB pep.*
8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB pep.*
9: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB pep.*
10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB pep.*
11: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB pep.*
12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB pep.*
13: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB pep.*
14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1239	100.0	242	10	US-09-989-903-5
2	1234	99.6	242	10	US-09-945-028-2
3	1194	96.4	242	10	US-09-764-803A-24
4	1189	96.0	242	10	US-09-845-028-9
5	1166	94.1	229	10	US-09-764-803A-4
6	1065	86.0	214	10	US-09-989-903-9
7	934.5	75.4	257	10	US-09-764-803A-2
8	934.5	75.4	260	10	US-09-989-903-2
9	890	71.8	230	10	US-09-989-903-7
10	295	23.8	451	10	US-09-888-243-28
11	293	23.6	74	10	US-09-989-903-63
12	289	23.3	435	10	US-09-954-697-9
13	273.5	22.1	277	10	US-09-895-263-4
14	272.5	22.0	264	9	US-10-103-448-3
15	272.5	22.0	264	9	US-10-108-929-3
16	272.5	22.0	277	10	US-09-954-697-12
17	256	20.7	303	10	US-09-944-851-2
18	256	20.7	303	10	US-09-954-697-24
19	252	20.3	303	10	US-09-895-263-2

20	251	20.3	505	10	US-09-888-243-5	Sequence 5, Appl1
21	248	20.0	479	10	US-09-952-768-2	Sequence 2, Appl1
22	248	20.0	479	10	US-09-954-697-33	Sequence 33, Appl1
23	247.5	20.0	479	10	US-09-888-243-6	Sequence 6, Appl1
24	247.5	20.0	466	10	US-09-952-768-4	Sequence 4, Appl1
25	246.5	19.9	286	10	US-09-862-915-1	Sequence 1, Appl1
26	246.5	19.9	479	10	US-09-410-194-20	Sequence 20, Appl1
27	246	19.9	479	10	US-09-954-697-27	Sequence 27, Appl1
28	245.5	19.8	503	10	US-09-888-243-29	Sequence 29, Appl1
29	239.5	19.3	416	9	US-10-068-569-1	Sequence 1, Appl1
30	232.5	18.8	416	9	US-10-059-749-2	Sequence 2, Appl1
31	232.5	18.8	416	10	US-09-954-697-30	Sequence 30, Appl1
32	226	18.2	383	10	US-09-764-803A-23	Sequence 23, Appl1
33	226	18.2	404	9	US-09-827-708A-2	Sequence 2, Appl1
34	226	18.2	404	10	US-09-954-697-6	Sequence 6, Appl1
35	225	18.2	404	10	US-09-888-243-30	Sequence 30, Appl1
36	225	18.2	418	10	US-09-954-697-18	Sequence 18, Appl1
37	222	17.9	293	10	US-09-954-697-21	Sequence 21, Appl1
38	221.5	17.9	354	10	US-09-888-243-20	Sequence 20, Appl1
39	221.5	17.9	503	10	US-09-888-243-2	Sequence 2, Appl1
40	221.5	17.9	521	10	US-09-962-834A-2	Sequence 2, Appl1
41	221.5	17.9	571	10	US-09-410-194-21	Sequence 21, Appl1
42	217.5	17.6	402	10	US-09-888-243-14	Sequence 14, Appl1
43	214	17.3	293	9	US-10-171-077-5	Sequence 5, Appl1
44	214	17.0	410	10	US-09-917-265-24	Sequence 24, Appl1
45	210.5	17.0	410	10	US-09-917-265-15	Sequence 15, Appl1

ALIGNMENTS

RESULT 1
US-09-989-903-5
Sequence 5, Application US/09989903
Patent No. US0020146804A1
GENERAL INFORMATION:
APPLICANT: Alnemi, Emd S.
TITLE OF INVENTION: Fernandez-Alnemi, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 460140.434D1
CURRENT FILING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapien
US-09-989-903-5

Query Match	100.0%	Score 1239	DB 10	Length 242
Best Local Similarity	100.0%	Pred. No. 6.8e-113		
Matches 242	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MSNPRSLSEEEKYDMSGALALILCTYKARSGSEEDLDLLEHMPOLRRESTMKRDPTAEQ	60	
DB	1	MSNPRSLSEEEKYDMSGALALILCTYKARSGSEEDLDLLEHMPOLRRESTMKRDPTAEQ	60	
QY	61	FOEELKEFOAIDSRDPVSCAFVVLMAHGREGLKSGDEGMVXLENLFEALNNKQCAL	120	
DB	61	FOEELKEFOAIDSRDPVSCAFVVLMAHGREGLKSGDEGMVXLENLFEALNNKQCAL	120	
QY	121	RAKPVYIYIACRGEORPGETVGDDELIVMVIKSPQITPYTDLAHYSTEVEGIAIYRHH	180	
DB	121	RAKPVYIYIACRGEORPGETVGDDELIVMVIKSPQITPYTDLAHYSTEVEGIAIYRHH	180	
QY	181	DOKSCFIQTLVDVFTTKKGIHLELTVTRMAEALVOGKARKTNPETOSTLRKLY	240	
DB	181	DOKSCFIQTLVDVFTTKKGIHLELTVTRMAEALVOGKARKTNPETOSTLRKLY	240	
QY	241	LQ 242		

Db 241 LQ 242

RESULT 2

US-09-845-028-2
 ; Sequence 2, Application US/09845028
 ; Patent No. US20020081705A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mankovich, John
 ; TITLE OF INVENTION: HUMAN CASPASE-14 COMPOSITIONS
 ; FILE REFERENCE: Bt-111
 ; CURRENT APPLICATION NUMBER: US/09/845,028
 ; CURRENT FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: 60/199,962
 ; PRIOR FILING DATE: 2000-04-27
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 242
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-845-028-2

Query Match 99.6%; Score 1234; DB 10; Length 242;
 Best Local Similarity 99.6%; Pred. No. 2.1e-112;
 Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRLSEEEKYDMSGALALILCVTKAREGSEEDLDALHMFROLRFESTMKRDPPTAQ 60
 Db 1 MSNPRLSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFROLRFESTMKRDPPTAQ 60
 QY 61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDEGVKLENLFEALNNKCOAL 120
 Db 61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDEGVKLENLFEALNNKCOAL 120
 QY 121 RAKPKVYIIQACRGQRDPGETVSGDEIWMVKDSPTIPTYTDLAHVYSTVEGYIAYRH 180
 Db 121 RAKPKVYIIQACRGQRDPGETVSGDEIWMVKDSPTIPTYTDLAHVYSTVEGYIAYRH 180
 QY 181 DOKGSCFIOTLVDFVTKRKHILLETVTTRMAEAEVQEGKARKTNPEIOSTLRKRLY 240
 Db 181 DOKGSCFIOTLVDFVTKRKHILLETVTTRMAEAEVQEGKARKTNPEIOSTLRKRLY 240
 QY 241 LQ 242
 Db 241 LQ 242

RESULT 3

US-09-764-803A-24
 ; Sequence 24, Application US/09764803A
 ; Patent No. US20020034812A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Van de Craen, Marc
 ; APPLICANT: Declercq, Wim
 ; APPLICANT: Vandenaebiele, Peter
 ; APPLICANT: Fiers, Walter
 ; TITLE OF INVENTION: NEW CASPASE HOMOLOGUE
 ; FILE REFERENCE: 2676-4661US
 ; CURRENT APPLICATION NUMBER: US/09/764,803A
 ; CURRENT FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: PCT/EP99/04939
 ; PRIOR FILING DATE: 1999-07-12
 ; PRIOR APPLICATION NUMBER: EP 9820242.6
 ; PRIOR FILING DATE: 1999-07-17
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO 24
 ; LENGTH: 242
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: misc_feature

; OTHER INFORMATION: Description of Artificial Sequence: predicted (genscan program) h
 ; OTHER INFORMATION: uman caspase-1
 ; US-09-764-803A-24

Query Match 96.4%; Score 1194; DB 10; Length 242;
 Best Local Similarity 97.1%; Pred. No. 1.6e-108;
 Matches 235; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 MSNPRLSEEEKYDMSGALALILCVTKAREGSEEDLDALHMFROLRFESTMKRDPPTAQ 60
 Db 1 MSNPRLSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFROLRFESTMKRDPPTAQ 60
 QY 61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDEGVKLENLFEALNNKCOAL 120
 Db 61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDEGVKLENLFEALNNKCOAL 120
 QY 121 RAKPKVYIIQACRGQRDPGETVSGDEIWMVKDSPTIPTYTDLAHVYSTVEGYIAYRH 180
 Db 121 RAKPKVYIIQACRGQRDPGETVSGDEIWMVKDSPTIPTYTDLAHVYSTVEGYIAYRH 180
 QY 181 DOKGSCFIOTLVDFVTKRKHILLETVTTRMAEAEVQEGKARKTNPEIOSTLRKRLY 240
 Db 181 DOKGSCFIOTLVDFVTKRKHILLETVTTRMAEAEVQEGKARKTNPEIOSTLRKRLY 240
 QY 241 LQ 242
 Db 241 LQ 242

RESULT 4

US-09-845-028-9
 ; Sequence 9, Application US/09845028
 ; Patent No. US20020081705A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mankovich, John
 ; TITLE OF INVENTION: HUMAN CASPASE-14 COMPOSITIONS
 ; FILE REFERENCE: Bt-111
 ; CURRENT APPLICATION NUMBER: US/09/845,028
 ; CURRENT FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: 60/199,962
 ; PRIOR FILING DATE: 2000-04-27
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 9
 ; LENGTH: 242
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-845-028-9

Query Match 96.0%; Score 1189; DB 10; Length 242;
 Best Local Similarity 99.6%; Pred. No. 4.9e-108;
 Matches 232; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 EKYDMSGALALILCVTKAREGSEEDLDALHMFROLRFESTMKRDPPTAQFOEELKFO 69
 Db 10 EKYDMSGARLALILCVTKAREGSEEDLDALHMFROLRFESTMKRDPPTAQFOEELKFO 69
 QY 70 QAIDSRDVPSCAFVVLMAHGREGLKGEDEGVKLENLFEALNNKCOALRAKPKVYII 129
 Db 70 QAIDSRDVPSCAFVVLMAHGREGLKGEDEGVKLENLFEALNNKCOALRAKPKVYII 129
 QY 130 QACRGQRDPGETVSGDEIWMVKDSPTIPTYTDLAHVYSTVEGYIAYRHDOXSCFIQ 189
 Db 130 QACRGQRDPGETVSGDEIWMVKDSPTIPTYTDLAHVYSTVEGYIAYRHDOXSCFIQ 189
 QY 190 TLVDVFTKRGKHILLETVTTRMAEAEVQEGKARKTNPEIOSTLRKRLYQ 242
 Db 190 TLVDVFTKRGKHILLETVTTRMAEAEVQEGKARKTNPEIOSTLRKRLYQ 242

RESULT 5

US-09-764-803A-4
 ; Sequence 4, Application US/09764803A

Patent No. US20020034812A1
GENERAL INFORMATION:
APPLICANT: Van de Craen, Marc
APPLICANT: Declercq, Wim
APPLICANT: Vandenaebale, Peter
APPLICANT: Fiers, Walter
TITLE OF INVENTION: NEW CASPASE HOMOLOGUE
FILE REFERENCE: 2676-466IUS
CURRENT APPLICATION NUMBER: US/09/764, 803A
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: PCT/EP99/04939
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: EP 98202422.6
PRIOR FILING DATE: 1999-07-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 229
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-803A-4

Query Match 94.1%; Score 1166; DB 10; Length 229;
Best Local Similarity 99.6%; Pred. No. 7.8e-106;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 MSGAALLILCVTKARESEEDLDLHMFROLRESTMKRDPPTAEQOELEKFOQAID 73
DB 1 MSGARLALILCVTKARESEEDLDLHMFROLRESTMKRDPPTAEQOELEKFOQAID 60
QY 74 SREDPVSCAFVVLMAHGREGLKSGDEGMVLENLFEALNNKNCALRAKRVYIIQACR 133
DB 61 SREDPVSCAFVVLMAHGREGLKSGDEGMVLENLFEALNNKNCALRAKRVYIIQACR 120
QY 134 GEQDPEGTGDEIVWYIKDSPOTIPYTDALHYSTVEGIYARHDQKSCFIQTLVD 193
DB 121 GEQDPEGTGDEIVWYIKDSPOTIPYTDALHYSTVEGIYARHDQKSCFIQTLVD 180
QY 194 VFTKRKGHILELTVTRMAEALVOEGKARKTNPEIQTSLRKRLYLQ 242
DB 181 VFTKRKGHILELTVTRMAEALVOEGKARKTNPEIQTSLRKRLYLQ 229

RESULT 6

US-09-989-903-9
Sequence 9, Application US/09989903
Patent No. US20020146804A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emed S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434D1
CURRENT APPLICATION NUMBER: US/09/989, 903
CURRENT FILING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 214
TYPE: PRT
ORGANISM: Homo sapiens
US-09-989-903-9

Query Match 86.0%; Score 1065; DB 10; Length 214;
Best Local Similarity 88.0%; Pred. No. 4.6e-96;
Matches 213; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MSNPRSLSEEEKYDMSGALALILCVTKARESEEDLDLHMFROLRESTMKRPTAQ 60
DB 1 MSNPRSLSEEEKYDMSGALALILCVTKARESEEDLDLHMFROLRESTMKRPTAQ 34
QY 61 FOEELKFOQAIDSRDPVSCAFVVLMAHGREGLKSGDEGMVLENLFEALNNKNCAL 120

DB 35 --EELEKFOQAIDSRDPVSCAFVVLMAHGREGLKSGDEGMVLENLFEALNNKNCAL 92
QY 121 RAKPKVYIIQACRGEQDPEGTGDEIVWYIKDSPOTIPYTDALHYSTVEGIYARH 180
DB 93 RAKPKVYIIQACRGEQDPEGTGDEIVWYIKDSPOTIPYTDALHYSTVEGIYARH 152
QY 181 DQKSCFIQTLVDVFTKRKGHILELTVTRMAEALVOEGKARKTNPEIQTSLRKRL 240
DB 153 DQKSCFIQTLVDVFTKRKGHILELTVTRMAEALVOEGKARKTNPEIQTSLRKRL 212
QY 241 LQ 242
DB 213 LQ 214

RESULT 7

US-09-764-803A-2
Sequence 2, Application US/09764803A
Patent No. US20020034812A1
GENERAL INFORMATION:
APPLICANT: Van de Craen, Marc
APPLICANT: Declercq, Wim
APPLICANT: Vandenaebale, Peter
APPLICANT: Fiers, Walter
TITLE OF INVENTION: NEW CASPASE HOMOLOGUE
FILE REFERENCE: 2676-466IUS
CURRENT APPLICATION NUMBER: US/09/764, 803A
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: PCT/EP99/04939
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: EP 98202422.6
PRIOR FILING DATE: 1999-07-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 257
TYPE: PRT
ORGANISM: Mus musculus
US-09-764-803A-2

Query Match 75.4%; Score 934.5; DB 10; Length 257;
Best Local Similarity 70.9%; Pred. No. 2.8e-83;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;

QY 1 MSNPRSLSEEEKYDMSGALALILCVTKARESEEDLDLHMFROLRESTMKRDPPTAQ 60
DB 5 MSDPQLOEERYDMSGALALILCVTKARESEEDLDLHMFROLRESTMKRDPPTAQ 64
QY 61 FOEELKFOQAIDSRDPVSCAFVVLMAHGREGLKSGDEGMVLENLFEALNNKNCAL 120
DB 65 FLEELDEFOQIIDWKEEYVSCAFVVLMAHGREGLKSGDEGMVLENLFEALNNKNCAL 124
QY 121 RAKPKVYIIQACRGEQDPEGTGDEIVWYIKDSPOTIPYTDALHY 168
DB 125 RAKPKVYIIQACRGEQDPEGTGDEIVWYIKDSPOTIPYTDALHY 183
QY 169 YSTVEGIYARHDQKSCFIQTLVDVFTKRKGHILELTVTRMAEALVOEGKARKTN 228
DB 184 YSTVEGIYARHDQKSCFIQTLVDVFTKRKGHILELTVTRMAEALVOEGKARKTN 243
QY 229 PEIQTSLRKRLYLQ 242
DB 244 PEIQTSLRKRLYLQ 257

RESULT 8

US-09-989-903-2
Sequence 2, Application US/09989903
Patent No. US20020146804A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emed S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING

QY 1 MSNPRSLSEEEKYDMSGALALILCVTKARESEEDLDLHMFROLRESTMKRPTAQ 60
DB 1 MSNPRSLSEEEKYDMSGALALILCVTKARESEEDLDLHMFROLRESTMKRPTAQ 34
QY 61 FOEELKFOQAIDSRDPVSCAFVVLMAHGREGLKSGDEGMVLENLFEALNNKNCAL 120

; TITLE OF INVENTION: AND METHODS OF USE
 ; FILE REFERENCE: 480140.434D1
 ; CURRENT APPLICATION NUMBER: US/09/989,903
 ; CURRENT FILING DATE: 2002-04-11
 ; NUMBER OF SEQ ID NOS: 78
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 260
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-989-903-2

Query Match 75.4%; Score 934.5; DB 10; Length 260;
 Best Local Similarity 70.9%; Pred. No. 2.8e-83;
 Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;

QY 1 MSNPRLSEEEKYDMSGALALILCTYKAREGSEEDDALEHMFROLPFESTMKRDPDTAQ 60
 DB 8 MSDPPLDEERYDMSGARLALILCTYKAREGSEEDDALEHMFROLPFESTMKRDPDTAQ 67
 QY 61 FOEELKFOQAIDSRDPVSCAFVVMAGRGSGFLKGEDEGEMVLELFEALNNKXQAL 120
 DB 68 FLEELDERFOQTIDNNEEPVSCAFVVMAGRGSGFLKGEDEGEMVLELFEALNNKXQAL 127
 QY 121 RAKPKVYIIQACRGGRDPE-----ETVGDDEIWMVIXDSPQITPTTDLAHV 168
 DB 128 RCKPKVYIIQACRGGRDPEELRGNEELGDEDELGDDE-VAVLKNPQSIPTTDLHI 186
 QY 169 YSTVGEYIAYRRDQKSCITQTLVDYFTKRGHILELLEVTYRRMAEALVQEGKARKTN 228
 DB 187 YSTVGEYIAYRRDQKSGFIQTLVDYFTKRGHILELLEVTYRRMAEALVQEGKARKTN 246
 QY 229 PEIQTSLRKRLYLQ 242
 DB 247 PEVQSTLRKRLYLQ 260

RESULT 9
 US-09-989-903-7
 ; Sequence 7, Application US/09989903
 ; Patent No. US20020146804A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alnemri, Emed S.
 ; APPLICANT: Fernandez-Alnemri, Teresa
 ; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
 ; TITLE OF INVENTION: AND METHODS OF USE
 ; FILE REFERENCE: 480140.434D1
 ; CURRENT APPLICATION NUMBER: US/09/989,903
 ; CURRENT FILING DATE: 2002-04-11
 ; NUMBER OF SEQ ID NOS: 78
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 230
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-989-903-7

Query Match 71.8%; Score 890; DB 10; Length 230;
 Best Local Similarity 99.4%; Pred. No. 5.1e-79;
 Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRLSEEEKYDMSGALALILCTYKAREGSEEDDALEHMFROLPFESTMKRDPDTAQ 60
 DB 1 MSNPRLSEEEKYDMSGARLALILCTYKAREGSEEDDALEHMFROLPFESTMKRDPDTAQ 60
 QY 61 FOEELKFOQAIDSRDPVSCAFVVMAGRGSGFLKGEDEGEMVLELFEALNNKXQAL 120
 DB 61 FOEELKFOQAIDSRDPVSCAFVVMAGRGSGFLKGEDEGEMVLELFEALNNKXQAL 120
 QY 121 RAKPKVYIIQACRGGRDPEETVGDDEIWMVIXDSPQITPTTDLAHVSTVGG 174
 DB 121 RAKPKVYIIQACRGGRDPEETVGDDEIWMVIXDSPQITPTTDLAHVSTVGG 174

RESULT 10
 US-09-888-243-28

; Sequence 28, Application US/09888243
 ; Patent No. US20020136714A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Horvitz, R. Robert
 ; APPLICANT: Yuan, Junying
 ; APPLICANT: Shih, Shai
 ; TITLE OF INVENTION: Relatedness of Human Interleukin-1beta
 ; TITLE OF INVENTION: Convertase Gene to a C. Elegans Cell Death Gene, Inhibitory
 ; FILE REFERENCE: 01997/211003
 ; CURRENT APPLICATION NUMBER: US/09/888,243
 ; CURRENT FILING DATE: 2001-06-22
 ; PRIOR APPLICATION NUMBER: US 09/083,662
 ; PRIOR FILING DATE: 1998-05-22
 ; PRIOR APPLICATION NUMBER: US 08/394,189
 ; PRIOR FILING DATE: 1995-02-24
 ; PRIOR APPLICATION NUMBER: US 08/282,211
 ; PRIOR FILING DATE: 1994-07-11
 ; PRIOR APPLICATION NUMBER: US 07/984,182
 ; PRIOR FILING DATE: 1992-11-20
 ; PRIOR APPLICATION NUMBER: US 07/897,788
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 28
 ; LENGTH: 451
 ; TYPE: PRT
 ; ORGANISM: Murine
 US-09-888-243-28

Query Match 23.8%; Score 295; DB 10; Length 451;
 Best Local Similarity 31.5%; Pred. No. 8e-21; Indels 36; Gaps 7;
 Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

QY 29 RGSEEDDALEHMFROLPFESTMKRDPDTAQFOEELKFOQAIDSRDPVSCAFVVM 88
 DB 218 RSGGVDDHTTLVTLFKLGGYNVHLVDQTAQEMQKLNFG-LPAHVVTSCV-VALLS 275
 QY 89 HGRSEFLKGEDEGEMVLELFEALNNKXQALRAKPKVYIIQACRGGRDPE----- 140
 DB 276 HVEGEGIVGDDKLTQLOVEFRLFDNANCPSLONKPKMFIOACRGDETRDGVDDQDGN 335
 QY 141 -----ETVGDDEIWMVIXDSPQITPTTDLAHVSTVGGYIAYRRDQKSCFIQTLV 192
 DB 336 HTQSPGCESDGKKEELMKR-----LPRSDMIGYACLGNAAMRNKRGSWYIEALT 390
 QY 193 DVFTKR--KGHILELLEVTYRRMAEALVQEGKARKTN-----PEIQTSLRKRLYL 241
 DB 391 QVFSERACDMHVDMLVKNALIKE-----REGYAGTERHRCCKEMSFYCSITLQQLYL 444

RESULT 11
 US-09-989-903-63

; Sequence 63, Application US/09989903
 ; Patent No. US20020146804A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alnemri, Emed S.
 ; APPLICANT: Fernandez-Alnemri, Teresa
 ; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
 ; TITLE OF INVENTION: AND METHODS OF USE
 ; FILE REFERENCE: 480140.434D1
 ; CURRENT APPLICATION NUMBER: US/09/989,903
 ; CURRENT FILING DATE: 2002-04-11
 ; NUMBER OF SEQ ID NOS: 78
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 63
 ; LENGTH: 74
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-989-903-63

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

US-10-103-448-1

Query Match 22.0%; Score 272.5; DB 9; Length 264;
Best Local Similarity 31.9%; Pred. No. 5.9e-19;
Matches 80; Conservative 39; Mismatches 103; Indels 29; Gaps 9;

Job time : 10.6414 secs

Qy 9 EEKYMSSGAALLILCVTK-----ARGESEEDLALHEMFROLFEESTMKRDPPTA 58
Db 21 DNSYKMDYPEWGLCTIINNKNFHKSTGMTSRSGTDVDAANLRETFPNLKYEVANKNDLTR 80
Qy 59 EFOFELEKFOQAIDSREDPVSCAFVILMAHGREGLKGEDG--EMVKLENLFEALNNKN 116
Db 81 BEIVELMRDVSKEDSHKSSFFVC---VLSHGEGLIIFGTNGPVDLKITNFF--RGDR 134
Qy 117 COALRAKPKVYIIQACRGEQRPDG--ETVGGDEIVWYIKDSPOTIPTYTDLAHVYSTVEGY 175
Db 135 CRSLTGKPKLFIQACRGTELDGIEITDSGVDDMAC---HKIPVDADFLYAYSTAPGY 190
Qy 176 IAYRHQKSGSCFIQTLVDVFTK--RKGHLLELLETVTRMA--EALVQ--EGKARKTNP 229
Db 191 YSWRNSKDSWFIQSICAMLKQYADKLEFPHILTRVNRKVATEFESFSPDATFHAQQIP 250
Qy 230 EIQSTLRKRLY 240
Db 251 CIVSMULTKELY 261

RESULT 15

US-10-108-929-3
; Sequence 3, Application US/10108929
; Publication No. US20020197702A1
; GENERAL INFORMATION:
; APPLICANT: Krebs, Joseph F.
; APPLICANT: Srinivasan, Anu
; APPLICANT: Fritz, Lawrence C.
; APPLICANT: Mu, Joseph C.
; TITLE OF INVENTION: MEMBRANE DERIVED CASPASE-3, COMPOSITIONS
; TITLE OF INVENTION: COMPRISING THE SAME AND METHODS OF USE THEREFOR
; FILE REFERENCE: 480140.468D2
; CURRENT APPLICATION NUMBER: US/10/108,929
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-108-929-3

Query Match 22.0%; Score 272.5; DB 9; Length 264;
Best Local Similarity 31.9%; Pred. No. 5.9e-19;
Matches 80; Conservative 39; Mismatches 103; Indels 29; Gaps 9;

Qy 9 EEKYMSSGAALLILCVTK-----ARGESEEDLALHEMFROLFEESTMKRDPPTA 58
Db 21 DNSYKMDYPEWGLCTIINNKNFHKSTGMTSRSGTDVDAANLRETFPNLKYEVANKNDLTR 80
Qy 59 EFOFELEKFOQAIDSREDPVSCAFVILMAHGREGLKGEDG--EMVKLENLFEALNNKN 116
Db 81 BEIVELMRDVSKEDSHKSSFFVC---VLSHGEGLIIFGTNGPVDLKITNFF--RGDR 134
Qy 117 COALRAKPKVYIIQACRGEQRPDG--ETVGGDEIVWYIKDSPOTIPTYTDLAHVYSTVEGY 175
Db 135 CRSLTGKPKLFIQACRGTELDGIEITDSGVDDMAC---HKIPVDADFLYAYSTAPGY 190
Qy 176 IAYRHQKSGSCFIQTLVDVFTK--RKGHLLELLETVTRMA--EALVQ--EGKARKTNP 229
Db 191 YSWRNSKDSWFIQSICAMLKQYADKLEFPHILTRVNRKVATEFESFSPDATFHAQQIP 250
Qy 230 EIQSTLRKRLY 240
Db 251 CIVSMULTKELY 261

Search completed: February 26, 2003, 12:28:00

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 26, 2003, 12:17:56 ; Search time 13.0159 Seconds
(without alignments)
547.048 Million cell updates/sec

Title: US-09-989-903-5
Perfect score: 1239
Sequence: 1 MSNPRSLSEEEKYDMSGALAL.....KARKTNPDIQSTLRKRLYLQ 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PTUG_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1239	100.0	242	US-09-187-789-5	Sequence 5, Appl
2	1065	86.0	214	US-09-187-789-9	Sequence 9, Appl
3	934.5	75.4	260	US-09-187-789-2	Sequence 2, Appl
4	934.5	75.4	260	US-09-139-600-2	Sequence 2, Appl
5	890	71.8	230	US-09-187-789-7	Sequence 7, Appl
6	293	23.6	74	US-09-187-789-63	Sequence 63, Appl
7	293	23.6	74	US-09-119-600-58	Sequence 58, Appl
8	289	23.3	421	US-08-983-502-10	Sequence 10, Appl
9	289	23.3	421	PCT-US96-10521-10	Sequence 10, Appl
10	289	23.3	435	US-08-258-287B-53	Sequence 53, Appl
11	289	23.3	435	US-08-368-704C-51	Sequence 51, Appl
12	289	23.3	435	US-09-561-756-9	Sequence 9, Appl
13	289	23.3	435	US-09-227-721-9	Sequence 9, Appl
14	289	23.3	435	US-08-816-075-2	Sequence 2, Appl
15	289	23.3	435	PCT-US94-07127A-4	Sequence 4, Appl
16	289	23.3	441	US-08-258-287B-44	Sequence 44, Appl
17	289	23.3	441	US-08-368-704C-43	Sequence 43, Appl
18	278.5	22.5	277	US-08-890-542A-2	Sequence 2, Appl
19	273.5	22.1	277	US-08-591-605-2	Sequence 2, Appl
20	273.5	22.1	277	US-08-964-308-6	Sequence 6, Appl
21	273.5	22.1	277	US-08-964-308-6	Sequence 4, Appl
22	273.5	22.1	277	US-08-462-969B-4	Sequence 4, Appl
23	273.5	22.1	277	US-08-964-313-6	Sequence 6, Appl
24	272.5	22.0	277	US-09-069-138-6	Sequence 6, Appl
25	272.5	22.0	277	US-09-561-756-12	Sequence 12, Appl
26	272.5	22.0	277	US-09-227-721-12	Sequence 12, Appl
27	272.5	22.0	277	US-08-983-502-30	Sequence 30, Appl
			277	PCT-US96-10521-30	Sequence 30, Appl

28	263.5	21.3	277	US-08-964-308-10	Sequence 10, Appl
29	263.5	21.3	277	US-08-964-313-10	Sequence 10, Appl
30	263.5	21.3	277	US-09-069-138-10	Sequence 10, Appl
31	257	20.7	503	US-08-258-287B-36	Sequence 36, Appl
32	257	20.7	503	US-08-368-704C-36	Sequence 36, Appl
33	256	20.7	303	US-09-561-756-24	Sequence 24, Appl
34	256	20.7	303	US-09-227-721-24	Sequence 24, Appl
35	256	20.7	303	US-08-556-627A-2	Sequence 2, Appl
36	252	20.3	303	US-08-462-969B-2	Sequence 2, Appl
37	251	20.3	505	US-08-394-189B-5	Sequence 5, Appl
38	251	20.3	505	PCT-US93-05701-20	Sequence 20, Appl
39	251	20.3	505	PCT-US93-05705-5	Sequence 5, Appl
40	249	20.1	497	US-08-258-287B-37	Sequence 37, Appl
41	249	20.1	497	US-08-368-704C-37	Sequence 37, Appl
42	248	20.0	346	US-08-618-408B-2	Sequence 2, Appl
43	248	20.0	479	US-08-665-220-2	Sequence 2, Appl
44	248	20.0	479	US-09-291-692-2	Sequence 2, Appl
45	248	20.0	479	US-09-561-756-33	Sequence 33, Appl

ALIGNMENTS

```

RESULT 1
US-09-187-789-5
: Sequence 5, Application US/09187789
: Patent No. 6340740
: GENERAL INFORMATION:
: APPLICANT: Alnemeti, Emed S.
: APPLICANT: Fernandez-Alnemeti, Teresa
: TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
: FILE REFERENCE: 480140.434C1
: CURRENT APPLICATION NUMBER: US/09/187, 789
: CURRENT FILING DATE: 1998-11-06
: NUMBER OF SEQ ID NOS: 78
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 5
: LENGTH: 242
: TYPE: PRT
: ORGANISM: Homo sapien
: US-09-187-789-5

Query Match      100.0%; Score 1239; DB 4; Length 242;
Best Local Similarity 100.0%; Pred No. 2.4e-122;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLDALHEMFRLRPFESTMKRDPTRAEQ 60
DQ      1 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLDALHEMFRLRPFESTMKRDPTRAEQ 60
DQ      61 FOEELERFOQAIIDREDPVSCAFVYLMAGHREGFLKGEDGMVLENUFELANNKNCQAL 120
QY      61 FOEELERFOQAIIDREDPVSCAFVYLMAGHREGFLKGEDGMVLENUFELANNKNCQAL 120
DQ      61 FOEELERFOQAIIDREDPVSCAFVYLMAGHREGFLKGEDGMVLENUFELANNKNCQAL 120
DQ      121 RAKKVVYIIONCRGEOBPGETVSGDEIVMWYIKDSPOTIPYTDALHYSTVEGIAYRH 180
QY      121 RAKKVVYIIONCRGEOBPGETVSGDEIVMWYIKDSPOTIPYTDALHYSTVEGIAYRH 180
DQ      121 RAKKVVYIIONCRGEOBPGETVSGDEIVMWYIKDSPOTIPYTDALHYSTVEGIAYRH 180
QY      181 DQKSCFQTLVDVFTKRKGHILLETVTTRMAEALVDEGKARKTNPDIQSTLRRLY 240
DQ      181 DQKSCFQTLVDVFTKRKGHILLETVTTRMAEALVDEGKARKTNPDIQSTLRRLY 240
QY      241 LQ 242
DQ      241 LQ 242

RESULT 2
US-09-187-789-9
: Sequence 9, Application US/09187789
: Patent No. 6340740
: GENERAL INFORMATION:

```

APPLICANT: Alnemri, Emed S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 214
TYPE: PRT
ORGANISM: Homo sapien
US-09-187-789-9

Query Match 86.0%; Score 1065; DB 4; Length 214;
Best Local Similarity 88.0%; Pred. No. 3.8e-104; Indels 28; Gaps 1;
Matches 213; Conservative 0; Mismatches 1;

QY 1 MSNPRLSEEEKYDMSGALALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPPTAQ 60
DB 1 MSNPRLSEEEKYDMSGARLALILCVTKAREGSE----- 34
QY 61 FOELEKFOQAIDSREDPVSCAFVYLMAGREGFLKGEDGEMVKLENLFEALNNKNCQAL 120
DB 35 --EELEKFOQAIDSREDPVSCAFVYLMAGREGFLKGEDGEMVKLENLFEALNNKNCQAL 92
QY 121 RAKPKVYIIQACRGORPGEIVGDEIWMVKDSPQITPTTDLAHVSTVEGYIAYRH 180
DB 93 RAKPKVYIIQACRGORPGEIVGDEIWMVKDSPQITPTTDLAHVSTVEGYIAYRH 152
QY 181 DQKSGCFIQTLDVFTKRGHILLETETVRMAEAEIVQEGKARKTNEIOSTLRKRLY 240
DB 133 DQKSGCFIQTLDVFTKRGHILLETETVRMAEAEIVQEGKARKTNEIOSTLRKRLY 212
QY 241 LQ 242
DB 213 LQ 214

RESULT 3
US-09-187-789-2
Sequence 2, Application US/09187789
Patent No. 6340740
GENERAL INFORMATION:
APPLICANT: Alnemri, Emed S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 260
TYPE: PRT
ORGANISM: Mus musculus
US-09-187-789-2

Query Match 75.4%; Score 934.5; DB 4; Length 260;
Best Local Similarity 70.9%; Pred. No. 2.6e-90;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;

QY 1 MSNPRLSEEEKYDMSGALALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPPTAQ 60
DB 8 MSNPRLSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPPTAQ 67
QY 61 FOELEKFOQAIDSREDPVSCAFVYLMAGREGFLKGEDGEMVKLENLFEALNNKNCQAL 120
DB 68 FLEELDEFQOTIDNMEBVSFAFVYLMAGREGFLKGEDGEMVKLENLFEALNNKNCQAL 127
QY 121 RAKPKVYIIQACRGORPGEIVGDEIWMVKDSPQITPTTDLAHV 168

DB 128 RGRKRVYIIQACRGHDPGEELRGNEELGDEELGDE--VAVLKNNPOSIPYTDLHI 186
QY 169 YSTVEGYIAYRHDOKSGCFIQTLDVFTKRGHILLETETVRMAEAEIVQEGKARKTN 228
DB 187 YSTVEGYIAYRHDOKSGCFIQTLDVFTKRGHILLETETVRMAEAEIVQEGKARKTN 246
QY 229 PEIOSTLRKRLYLQ 242
DB 247 PEIOSTLRKRLYLQ 260

RESULT 4
US-09-139-600-2
Sequence 2, Application US/09139600
Patent No. 643628
GENERAL INFORMATION:
APPLICANT: Alnemri, Emed S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHOD OF USE
FILE REFERENCE: 480140.434
CURRENT APPLICATION NUMBER: US/09/139,600
CURRENT FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 260
TYPE: PRT
ORGANISM: Mus musculus
US-09-139-600-2

Query Match 75.4%; Score 934.5; DB 4; Length 260;
Best Local Similarity 70.9%; Pred. No. 2.6e-90;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;

QY 1 MSNPRLSEEEKYDMSGALALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPPTAQ 60
DB 8 MSNPRLSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFQRLRFESTMKRDPPTAQ 67
QY 61 FOELEKFOQAIDSREDPVSCAFVYLMAGREGFLKGEDGEMVKLENLFEALNNKNCQAL 120
DB 68 FLEELDEFQOTIDNMEBVSFAFVYLMAGREGFLKGEDGEMVKLENLFEALNNKNCQAL 127
QY 121 RAKPKVYIIQACRGORPGEIVGDEIWMVKDSPQITPTTDLAHV 168
DB 128 RAKPKVYIIQACRGHDPGEELRGNEELGDEELGDE--VAVLKNNPOSIPYTDLHI 186
QY 169 YSTVEGYIAYRHDOKSGCFIQTLDVFTKRGHILLETETVRMAEAEIVQEGKARKTN 228
DB 187 YSTVEGYIAYRHDOKSGCFIQTLDVFTKRGHILLETETVRMAEAEIVQEGKARKTN 246
QY 229 PEIOSTLRKRLYLQ 242
DB 247 PEIOSTLRKRLYLQ 260

RESULT 5
US-09-187-789-7
Sequence 7, Application US/09187789
Patent No. 6340740
GENERAL INFORMATION:
APPLICANT: Alnemri, Emed S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 230

TYPE: PRT
ORGANISM: Homo sapien
US-09-187-789-7

Query Match 71.8%; Score 890; DB 4; Length 230;
Best Local Similarity 99.4%; Pred. No. 1e-85;
Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNRSLEEKYDMSGALALILCTKAREGSEEDLDALHEMFRLPFESTMKDPTAEQ 60
DB 1 MSNPSLEEEKYDMSGALALILCTKAREGSEEDLDALHEMFRLPFESTMKDPTAEQ 60
QY 61 FOELEKFOAIDSRDPVSCAFVLMAGREGFLKGEDEGMVLENLFEALNNKCOAL 120
DB 61 FOELEKFOAIDSRDPVSCAFVLMAGREGFLKGEDEGMVLENLFEALNNKCOAL 120
QY 121 RAKPKYIIQACRGQDPGRTVGDEIVWIKSPQTIPTTALHVSIVEG 174
DB 121 RAKPKYIIQACRGQDPGRTVGDEIVWIKSPQTIPTTALHVSIVEG 174

RESULT 6
US-09-187-789-63

Sequence 63, Application US/09187789

Patent No. 6340740

GENERAL INFORMATION:

APPLICANT: Alnemri, Emdad S.

APPLICANT: Fernandez-Alnemri, Teresa

TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING

FILE REFERENCE: 480140.434C1

CURRENT APPLICATION NUMBER: US/09/187,789

CURRENT FILING DATE: 1998-11-06

NUMBER OF SEQ ID NOS: 78

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 63

LENGTH: 74

TYPE: PRT

ORGANISM: Mus musculus

US-09-187-789-63

Query Match 23.6%; Score 293; DB 4; Length 74;
Best Local Similarity 77.8%; Pred. No. 1.1e-23;
Matches 56; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 28 ARSESEDLALHEMFRLPFESTMKDPTAEQFOELEKFOAIDSRDPVSCAFVLM 87
DB 1 ARSESEVDMELERMFRLPFESTMKDPTAEQFLBELDFQOTIDWEEBVSACAFVLM 60

QY 88 AHGREGFLKGED 99
DB 61 AHGREGFLKGED 72

RESULT 7
US-09-139-600-58

Sequence 58, Application US/09139600

Patent No. 6432628

GENERAL INFORMATION:

APPLICANT: Alnemri, Emdad S.

APPLICANT: Fernandez-Alnemri, Teresa

TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING

FILE REFERENCE: 460140.434

CURRENT APPLICATION NUMBER: US/09/139,600

CURRENT FILING DATE: 1998-08-25

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 58

LENGTH: 74

TYPE: PRT

ORGANISM: Mus musculus

US-09-139-600-58

Query Match 23.6%; Score 293; DB 4; Length 74;
Best Local Similarity 77.8%; Pred. No. 1.1e-23;
Matches 56; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 28 ARSESEDLALHEMFRLPFESTMKDPTAEQFOELEKFOAIDSRDPVSCAFVLM 87
DB 1 ARSESEVDMELERMFRLPFESTMKDPTAEQFLBELDFQOTIDWEEBVSACAFVLM 60
QY 88 AHGREGFLKGED 99
DB 61 AHGREGFLKGED 72

RESULT 8
US-08-983-502-10

Sequence 10, Application US/08983502

Patent No. 639327

GENERAL INFORMATION:

APPLICANT: David WALLACH

APPLICANT: Mark P. BOLDIN

APPLICANT: Tanya M. GONCHAROV

APPLICANT: Yuri V. GOLITSEV

TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Broadway and Neimark

STREET: 419 Seventh Street N.W., Ste. 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/983,502

FILING DATE: 16-JAN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/10521

FILING DATE: 14-JUN-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 114,615

FILING DATE: 16-JUL-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 114,986

FILING DATE: 17-AUG-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 115,319

FILING DATE: 14-SEP-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 116,588

FILING DATE: 27-DEC-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 117,932

FILING DATE: 16-APR-1996

PRIOR APPLICATION DATA:

NAME: Broadway, Roger L.

REGISTRATION NUMBER: 25,618

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-5197

TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 421 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-983-502-10

Query Match 23.3%; Score 289; DB 4; Length 421;
Best Local Similarity 31.1%; Pred. No. 3.5e-22;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

QY 29 REGSEEDLDALHMFROQLFESTMKRDPPTAEQFOEELKFOQAIDSREDPVSCAFVYMA 88
DB 188 RSGGVDHSTLVTLFLKLGVDVHVLCDQTAQEMQEKLNFAQ-LPAHRTVDS-C-IVALIS 245
QY 89 HGREGLKGEDEGMVYKLELFEALNNKQCALRAKPKVYIIQACRGEQDPG----- 140
DB 246 HVEGAIVGVDPKLLQLOEVFQLFDNANCPSLQNKPKMFFIQACRGDETRDGVQDQDGN 305
QY 141 -----ETVGGDEIVWVITKDSPTIPTYDALHVSIVVEGYIAYRHDOXGSCFIOTLV 192
DB 306 HAGSPGCEESDAGKE-----KLPPKRLPTRSDMTCGYACLGTAAMRTKRGSWYTEALA 360
QY 193 DVFTKR--KGHLELLEVTTRMAEALVQEGKARKTN-----PEIOSTLRKRLYL 241
DB 361 QVFSERACDMHVDMLVKNALIKD----REGYAPGTEFHCKMSEYCSITLCHRLYL 414

RESULT 9
PCT-US96-10521-10
Sequence 10, Application PC/TUS9610521
GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
TITLE OF INVENTION: AND OTHER PROTEINS
NUMBER OF SEQUENCES: 34
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10521-10

Query Match 23.3%; Score 289; DB 5; Length 421;
Best Local Similarity 31.1%; Pred. No. 3.5e-22;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

QY 29 REGSEEDLDALHMFROQLFESTMKRDPPTAEQFOEELKFOQAIDSREDPVSCAFVYMA 88
DB 188 RSGGVDHSTLVTLFLKLGVDVHVLCDQTAQEMQEKLNFAQ-LPAHRTVDS-C-IVALIS 245
QY 89 HGREGLKGEDEGMVYKLELFEALNNKQCALRAKPKVYIIQACRGEQDPG----- 140

DB 246 HVEGAIVGVDPKLLQLOEVFQLFDNANCPSLQNKPKMFFIQACRGDETRDGVQDQDGN 305
QY 141 -----ETVGGDEIVWVITKDSPTIPTYDALHVSIVVEGYIAYRHDOXGSCFIOTLV 192
DB 306 HAGSPGCEESDAGKE-----KLPPKRLPTRSDMTCGYACLGTAAMRTKRGSWYTEALA 360
QY 193 DVFTKR--KGHLELLEVTTRMAEALVQEGKARKTN-----PEIOSTLRKRLYL 241
DB 361 QVFSERACDMHVDMLVKNALIKD----REGYAPGTEFHCKMSEYCSITLCHRLYL 414

RESULT 10
US-08-258-287B-53
Sequence 53, Application US/08258287B
Patent No. 6083735
GENERAL INFORMATION:

APPLICANT: Yuan, Junyong
APPLICANT: Mura, Masayuki
TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,287B
FILING DATE: 10-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/080,850
FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609,3920001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-258-287B-53

Query Match 23.3%; Score 289; DB 3; Length 435;
Best Local Similarity 31.1%; Pred. No. 3.6e-22;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

QY 29 REGSEEDLDALHMFROQLFESTMKRDPPTAEQFOEELKFOQAIDSREDPVSCAFVYMA 88
DB 202 RSGGVDHSTLVTLFLKLGVDVHVLCDQTAQEMQEKLNFAQ-LPAHRTVDS-C-IVALIS 259
QY 89 HGREGLKGEDEGMVYKLELFEALNNKQCALRAKPKVYIIQACRGEQDPG----- 140
DB 260 HVEGAIVGVDPKLLQLOEVFQLFDNANCPSLQNKPKMFFIQACRGDETRDGVQDQDGN 319
QY 141 -----ETVGGDEIVWVITKDSPTIPTYDALHVSIVVEGYIAYRHDOXGSCFIOTLV 192
DB 320 HAGSPGCEESDAGKE-----KLPPKRLPTRSDMTCGYACLGTAAMRTKRGSWYTEALA 374
QY 193 DVFTKR--KGHLELLEVTTRMAEALVQEGKARKTN-----PEIOSTLRKRLYL 241

Db 375 QVSEBRACDMHVAIDLKVDLVAALIKD---REGYAPGTEFFHRCCKEMSEYCSITLCHNLYL 428

RESULT 11
US-08-368-704C-51

; Sequence 51, Application US/08368704C
; Patent No. 6087160
; GENERAL INFORMATION:
; APPLICANT: Yuan, Junyang
; APPLICANT: Miura, Masayuki
; TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/368,704C
; FILING DATE: 4-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/258,287
; FILING DATE: 10-JUN-1994
; CLASSIFICATION: 435
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/080,850
; FILING DATE: 24-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0609,3920002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; TELEX: 248636 SSK
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-368-704C-51

Query Match 23.3%; Score 289; DB 3; Length 435;
Best Local Similarity 31.1%; Pred. No. 3.6e-22;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

QY 29 REGSEEDLALHEMFROLRESTKRDPTAEOFOELEKFOQALDSREDPVSCAFVVLMA 88
DB 202 RSGGDVHSTLVTLFKLGDVHVLCDQTAQEMQEKQNFQO-LPARHVTDSC-IVALLS 259
QY 89 HGREGFLKGEDGVKLENTFEALNNKQCALRAKPKVYIIQACRGEORDPG----- 140
DB 260 HGVEGAIYGVNDKQLQOEIVFQFDNANCPSLQNKPKMFIQACRGDETRDGVQDOQGN 319
QY 141 -----ETVGGDEIVMWIKDSQPTIPTYTDLAHVISTVEGYIAYRHDDQKSCFIOTLV 192
DB 320 HAGSPGCEESDAGE-----KLPRKRLPTRSDMTCGYACLGTAAMRTKRGSWYIEALA 374
QY 193 DVFTKR--KGHILELLEVTFRMAELVQEGKARKTN-----PEIQTLLRKRLYL 241
DB 375 QVSEBRACDMHVAIDLKVDLVAALIKD---REGYAPGTEFFHRCCKEMSEYCSITLCHNLYL 428

RESULT 12
US-09-561-756-9

; Sequence 9, Application US/09561756
; Patent No. 6376226
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/561,756
; CURRENT FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 09/227,721
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-561-756-9

Query Match 23.3%; Score 289; DB 4; Length 435;
Best Local Similarity 31.1%; Pred. No. 3.6e-22;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

QY 29 REGSEEDLALHEMFROLRESTKRDPTAEOFOELEKFOQALDSREDPVSCAFVVLMA 88
DB 202 RSGGDVHSTLVTLFKLGDVHVLCDQTAQEMQEKQNFQO-LPARHVTDSC-IVALLS 259
QY 89 HGREGFLKGEDGVKLENTFEALNNKQCALRAKPKVYIIQACRGEORDPG----- 140
DB 260 HGVEGAIYGVNDKQLQOEIVFQFDNANCPSLQNKPKMFIQACRGDETRDGVQDOQGN 319
QY 141 -----ETVGGDEIVMWIKDSQPTIPTYTDLAHVISTVEGYIAYRHDDQKSCFIOTLV 192
DB 320 HAGSPGCEESDAGE-----KLPRKRLPTRSDMTCGYACLGTAAMRTKRGSWYIEALA 374
QY 193 DVFTKR--KGHILELLEVTFRMAELVQEGKARKTN-----PEIQTLLRKRLYL 241
DB 375 QVSEBRACDMHVAIDLKVDLVAALIKD---REGYAPGTEFFHRCCKEMSEYCSITLCHNLYL 428

RESULT 13

; Sequence 9, Application US/09227721
; Patent No. 6379950
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/227,721
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-227-721-9

Query Match 23.3%; Score 289; DB 4; Length 435;
Best Local Similarity 31.1%; Pred. No. 3.6e-22;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

QY 29 REGSEEDLALHEMFROLRESTKRDPTAEOFOELEKFOQALDSREDPVSCAFVVLMA 88
DB 202 RSGGDVHSTLVTLFKLGDVHVLCDQTAQEMQEKQNFQO-LPARHVTDSC-IVALLS 259
QY 89 HGREGFLKGEDGVKLENTFEALNNKQCALRAKPKVYIIQACRGEORDPG----- 140
DB 260 HGVEGAIYGVNDKQLQOEIVFQFDNANCPSLQNKPKMFIQACRGDETRDGVQDOQGN 319

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QY      141 -----ETVGGGEIVAVIDSPQTITFDALHVVSTVGATVAHDGSGEICTLV 192
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      320 HAGSCCESSAGNE-----KLPKRLEPTSDWI CGVACLKGTAAMENTRKGSMTIALA 374
QY      193 DVFETR--KGIIELTVEVTRRMAAEIIVCGSKARKN-----PELTSLRRLYL 241
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      375 QVFSEKACDMHVADHLVKNAALIKD---RGGYAPGLEFPHCKEMSEYCSLTCCHLYL 428

```

RESULT 14
 US-08-816-075-2
 : Sequence 2, Application US/08816075
 : Patent No. 6416753
 :
 : GENERAL INFORMATION:
 : APPLICANT: Yuan, Junying
 : APPLICANT: Friedlander, Robert
 : TITLE OF INVENTION: Programmed Cell Death and Interleukin-1
 : NUMBER OF SEQUENCES: 3
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 : STREET: 1100 New York Ave., N.W.
 : CITY: Washington
 : STATE: DC
 : COUNTRY: USA
 : ZIP: 20005
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 :
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/816,075
 : FILING DATE: 13-MAR-1997
 : CLASSIFICATION: 424
 :
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 60/013,524
 : FILING DATE: 15-MAR-1996
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Bugalsky, Lawrence B.
 : REGISTRATION NUMBER: 35,086
 : REFERENCE/DOCKET NUMBER: 0609.421001/JAG/LBB
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 202-371-2650
 : TELEFAX: 202-371-2540
 : INFORMATION FOR SEQ ID NO: 2:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 435 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 :
 : MOLECULE TYPE: protein
 :
 : US-08-816-075-2

Query Match	23.3%;	Score 289;	DB 4;	Length 435;
Best Local Similarity	31.1%;	Pred. No. 3.6e-22;		
Matches	74;	Conservative	51;	Mismatches 77;
				Indels 36;
				Gaps 7;

[illegible]

RESULT 15
 PCT-US94-07127A-4
 Sequence 4, Application PC/TUS9407127A
 GENERAL INFORMATION:
 APPLICANT: HE, ET AL.
 TITLE OF INVENTION: Interleukin-1 Converting Enzyme Like Apoptosis Protease-1, and
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
 ADDRESSEE: CECCHI, STEWART & OLSTEIN
 STREET: 6 BECKER FARM ROAD
 CITY: ROSELAND
 STATE: NEW JERSEY
 COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 INCH DISKETTE
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/07127A
 FILING DATE: submitted herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: FERRARO, GREGORY D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325600-184
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 435 AMINO ACIDS
 TYPE: AMINO ACID
 STRANDEDNESS:
 TOPOLOGY: LINEAR 2
 MOLECULE TYPE: PROTEIN
 PCT-US94-07127A-4

Query Match	23.3%	Score 289;	DB 5;	Length 435;
Best Local Similarity	31.1%	Pred. No. 3.6e-22;		
Matches 74;	Conservative 51;	Mismatches 77;	Indels 36;	Gaps 7;

```

QY 29 REGSESDIDALEHNFPROLRFESTIKRPTLPAOFEELEKEQOALDSHEDSVSCAFVLLA 88
Db 202 RSGGDVDSHTLVTLFKLLGVVHVHLCQTOAEMOEKIQNFAQ-LPARHVDSCLVALLS 259
QY 89 HGREGFLKGDGDEWVUKLENLEFALNNKNCQALRAKPKVYIIQACRSHORDPG----- 140
Db 260 HGVBEALITGVDDQKLLQIQGVFQLFDNANCPBLQKPKMFFIQACRGPDETRGVDDQDKN 319
QY 141 -----ETWGGDEIVWVYKDSQOTIPTYDIALHYSTVBGYIAYNHDKGSGFIOTLV 192
Db 320 HAGSGCEPSDAGKE-----KLPRKRLPTRBDMICGACLKGTAMNTKRGSVYIEALA 374
QY 193 DVFETR--KGHLELLEVTNRMAEALVQSGARKYN-----PEIOTSLRRLVY 241
Db 375 QVFSRSGCDMHVADMLVKNALIKD---RGVAPGTBPHRCKMSMEYSTCLCRHLYL 428

```

Search completed: February 26, 2003, 12:22:04
Job time : 14.0159 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 26, 2003, 12:16:30 ; Search time 26.0319 Seconds
(without alignments)
1915.475 Million cell updates/sec

Title: US-09-989-903-5
Perfect score: 1239
Sequence: 1 MSNPRSLSEEKYDMGNAL.....KARKTPEIQSTLRKRLYLQ 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	293	23.6	452	11	O55194
2	289.5	23.4	423	13	O91B67
3	289	23.3	435	4	O9BUP7
4	284.5	23.0	283	13	O93417
5	274.5	22.2	277	6	O95ND5
6	274.5	22.2	383	13	O919L7
7	273.5	22.1	220	11	O9QW14
8	273.5	22.1	277	4	O96ANI
9	272	22.0	399	13	O91B63
10	270.5	21.8	277	4	O96KP2
11	270	21.8	303	11	O98550
12	269.5	21.8	454	11	O9R0T0
13	269	21.7	482	13	O90W11
14	266.5	21.5	282	13	O98U18
15	260.5	21.0	403	13	O90WU0
16	257	20.7	476	13	O91B73

17	256	20.7	500	13	O91B64	O91B64 xenopus lae
18	256	20.7	520	13	O91B62	O91B62 xenopus lae
19	255	20.6	417	5	O9YIU6	O9YIU6 pristionchu
20	254.5	20.5	454	11	O9JHK1	O9JHK1 ractus norv
21	250.5	20.2	318	13	O91B65	O91B65 xenopus lae
22	248.5	20.1	496	4	O9COK4	O9COK4 homo sapien
23	248	20.0	479	4	O8WYQ8	O8WYQ8 homo sapien
24	246.5	19.9	538	4	O8TD15	O8TD15 homo sapien
25	242.5	19.6	276	11	O9D089	O9D089 mus musculu
26	241.5	19.5	276	11	O9SM47	O9SM47 mus musculu
27	239.5	19.3	416	4	O9B062	O9B062 homo sapien
28	235.5	19.0	182	6	O77623	O77623 ovib aries
29	235	19.0	277	11	O35397	O35397 ractus norv
30	233	18.8	480	11	O89110	O89110 m caspase 8
31	230.5	18.6	482	11	O9JHX4	O9JHX4 ractus norv
32	228.5	18.4	347	5	O9GV89	O9GV89 hydra atten
33	228.5	18.4	404	13	O9PDJ2	O9PDJ2 brachydantio
34	225	18.2	308	5	O9NHF9	O9NHF9 drosophila
35	225	18.2	308	5	O9VET9	O9VET9 drosophila
36	223.5	18.0	326	5	O9GV88	O9GV88 hydra atten
37	222	17.9	293	4	O9BOE7	O9BOE7 homo sapien
38	220.5	17.8	304	13	O93415	O93415 gallus gall
39	220	17.8	283	13	O42284	O42284 gallus gall
40	219.5	17.7	402	11	O91W32	O91W32 ractus norv
41	217.5	17.6	303	13	O91B66	O91B66 xenopus lae
42	211.5	17.1	393	11	O9R0S9	O9R0S9 mus musculu
43	211	17.0	373	11	O91XW7	O91XW7 ractus norv
44	210.5	17.0	302	13	O91B59	O91B59 oncorhynch
45	210.5	17.0	826	5	O9Y055	O9Y055 caenorhabdi

ALIGNMENTS

RESULT 1
O55194 ID O55194 PRELIMINARY; PRT; 452 AA.
AC O55194; 01-JUN-1998 (TRENBLER, 06, Created)
DT 01-JUN-1998 (TRENBLER, 06, Last sequence update)
DE 01-MAR-2002 (TRENBLER, 20, Last annotation update)
BT NEBD2/ICH-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98087427; PubMed=9427555;
RA Sato N., Milligan C.E., Uchiyama Y., Oppenheim R.W.;
RT "Cloning and expression of the cDNA encoding rat caspase-2.";
RL Gene 202:127-132(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RA Jin K.L., Simon R.P., Graham S.H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; U77933; AAB96379.1; -.
DR EMBL; AF136231; AAD33684.1; -.
DR HSSP; P29466; 1ICE.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002318; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00655; ICE_P10; 1.
DR Pfam; PF00656; ICE_P20; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CARD; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.

DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 SQ SEQUENCE 452 AA; 50728 MW; 03F9D096B8741CE3 CRC64;

Query Match 23.6%; Score 293; DB 11; Length 452;
 Best Local Similarity 31.5%; Pred. No. 1.4e-16;
 Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

OY REGSEEDLDALHEMFRQLRFESTMKRDPFAEQFOEELKFOQAIDSRDPVSCAFVMA 88
 DB RSGGVDDHTLTTLTKLGYNVHLYDQTAQEMOKLQNFQA-LPAHRTDSC-IVALIS 276
 OY HGREGFLKGEDEGMVLENTFEALNNKNCQALRAKPKVYIIQACRGEORDPG----- 140
 DB HVEGEGIVGVDKLLQLOEVFRLFDNANCPSLQNKPKMFIIQACRGDETRGVDDQDGN 336
 OY 141 -----ETVGDDEIVWYIKDSPQITPTTDLAHVYSTVEGIYARRHQKSCFIQTLV 192
 DB 337 HAQSPGCESSDAGKEELMKMR-----LPTPSDMIICGYACLKGNAMRNKRGSWYTEALT 391
 OY 193 DVFTKR--KGHILELLTEVTRMAEAELVQEGKARKTN-----PEIQSTRKRLYL 241
 DB 332 QVFSERACDMHVAIDLKVNALIKE-----REGYAPGTETFRCKEMSEYCTLCQRLYL 445

RESULT 2

O91B67 PRELIMINARY; PRT; 423 AA.
 ID O91B67
 AC O91B67
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Caspase-2.
 GN XCAPASE-2.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20209426; PubMed=10744739;
 RA Nakajima K., Takahashi A., Yaoita Y.;
 RT "Structure, expression and function of the Xenopus laevis caspase
 RT family";
 RL J. Biol. Chem. 275:10484-10491(2000).
 DR EMBL; AB038168; BAA94746.1; --
 DR HSSP; P29466; 1ICE.
 DR MEROPS; C14.006; --
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR002398; ICE.
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00655; ICE_P10; 1.
 DR Pfam; PF00656; ICE_P20; 1.
 DR PRINTS; PR00376; ILIBENZYM.
 DR SMART; SM00114; CARD; 1.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS0209; CARD; 1.
 DR PROSITE; PS0122; CASPASE_CYS; 1.
 DR PROSITE; PS0121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 SQ SEQUENCE 423 AA; 47123 MW; E91BBLFD133F01FD CRC64;

Query Match 23.4%; Score 289.5; DB 13; Length 423;
 Best Local Similarity 30.5%; Pred. No. 2.6e-16;
 Matches 74; Conservative 51; Mismatches 71; Indels 47; Gaps 7;

OY 29 REGSEEDLDALHEMFRQLRFESTMKRDPFAEQFOEELKRF-----QQAIDSRDPVSCAF 83
 DB 187 RCGGEVDLSTLEKLFESLGYVDVRCNLNAGSMQSOLGAFSALPVSALDS-----CV 239

OY VLMAGREGFLKGEDEGMVLENTFEALNNKNCQALRAKPKVYIIQACRGEORDPG--- 140
 DB VAILSHGIDGAVYGTGDKLVQLOEVFTALDNACHPQLQNKPKMFIIQACRGEETDRGVDDQ 299
 OY 141 -----ETVGDDEIVWYIKDSPQITPTTDLAHVYSTVEGIYARRHQKSCFI 187
 DB 300 RDGREGSPGCEQSDARERIKV-----RLPTQSDMICVACLKGTVSJLNTKRGSWF 353
 OY 188 IOTLVDPFTK--RKHILELLTEVTRMAEAELVQEGKARKTN-----PEIQSTRKR 238
 DB 334 VQDLVSVFSQSHKQDTHVADMLKVNALIKE-----REGYAPGTETFRCKEMSEYCTLCRD 409
 OY 239 LYL 241
 DB 410 LYL 412

RESULT 3

O9BUP7 PRELIMINARY; PRT; 435 AA.
 ID O9BUP7
 AC O9BUP7
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Similar to caspase 2.
 DE Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Straube R.;
 RC TISSUE=SKIN;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC002427; AA02427.1; --
 DR HSSP; P29466; 1ICE.
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR002398; ICE.
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00655; ICE_P10; 1.
 DR Pfam; PF00656; ICE_P20; 1.
 DR PRINTS; PR00376; ILIBENZYM.
 DR SMART; SM00114; CARD; 1.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS0209; CARD; 1.
 DR PROSITE; PS0122; CASPASE_CYS; 1.
 DR PROSITE; PS0121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 SQ SEQUENCE 435 AA; 48869 MW; 10CFASALP9369E57 CRC64;

Query Match 23.3%; Score 289; DB 4; Length 435;
 Best Local Similarity 31.1%; Pred. No. 2.9e-16;
 Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

OY 29 REGSEEDLDALHEMFRQLRFESTMKRDPFAEQFOEELKFOQAIDSRDPVSCAFVMA 88
 DB 202 RSGGVDDHTLTTLTKLGYDVHLYDQTAQEMOKLQNFQA-LPAHRTDSC-IVALIS 259
 OY HGREGFLKGEDEGMVLENTFEALNNKNCQALRAKPKVYIIQACRGEORDPG----- 140
 DB HVEGEGIVGVDKLLQLOEVFRLFDNANCPSLQNKPKMFIIQACRGDETRGVDDQDGN 319
 OY 141 -----ETVGDDEIVWYIKDSPQITPTTDLAHVYSTVEGIYARRHQKSCFIQTLV 192
 DB 320 HAQSPGCESSDAGKE-----KLPKRLPTPSDMIICGYACLKGTAMRNKRGSWYTEALTA 374
 OY 193 DVFTKR--KGHILELLTEVTRMAEAELVQEGKARKTN-----PEIQSTRKRLYL 241
 DB 375 QVFSERACDMHVAIDLKVNALIKD-----REGYAPGTETFRCKEMSEYCTLCRRLYL 428

RESULT 4

093417 PRELIMINARY; PRT; 283 AA.
 AC 093417;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Caspase-3.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NC NCBI_TaxId=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20149872; PubMed=10684799;
 RA Johnson A.L., Bridgham J.T.,
 RT "Caspase-3 and -6 expression and enzyme activity in hen granulosa
 cells";
 RL Biol. Reprod. 62:589-598(2000).
 DR EMBL; AF083029; AAC32602.1; --.
 DR HSSP; P42574; IPAU.
 DR MEROPS; C14.003; --.
 DR InterPro; IPR002398; ICE.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR Pfam; PF00655; ICE_p10; 1.
 DR Pfam; PF00656; ICE_p20; 1.
 DR PRINTS; PR00376; ILIBENZYM.
 DR SMART; SM00115; CASP; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 SQ SEQUENCE 283 AA; 31675 MW; 161242DDEFD4DC4F CRC64;

Query Match 23.0%; Score 284.5; DB 13; Length 283;
 Best Local Similarity 30.3%; Pred. No. 4.2e-16;
 Matches 76; Conservative 47; Mismatches 101; Indels 27; Gaps 7;

QY 7 LEEERYDMSGALALILCVT-----KAREGSEDLALHEMFRLRFEFTMKRDP 56
 DB 40 LPDSSYRNDYDEIGCVIINKNFHRTGLSSRSTADASVREVFMKLGKVLNLDL 99
 QY 57 TAEPQOELEKFOAIDSREDPVSCAFVYLMAGREGFLKGEDEGMVKTENLFEALNNK 116
 DB 100 SSRDIFKLKRVSEEDHKSRSFVC---VLISHGDEGLFYGTDPFL-ELKVLTSLSFRGDK 155
 QY 117 COALRAKPKVYIIACRGEGRDPG--ETVGGDEIVMVIKDSPTPIPTVDALHYSTVEG 174
 DB 156 CRSLAGKRLKLFIOACRGTELDGSEADSGDETVC-----QKTPVADFLVYSTAPG 209
 QY 175 YIAVRHDKGSCFIQTLDVFTK--RKGHILELLEVTNRMAEALV---QEGKARKTNP 229
 DB 210 YYSWRNMAEGSWFIQSLCRLMKLKHARKLELMQILTRVNRVAVEYSSCTRODPNAKKQIP 269
 QY 230 EIGSTLRKRLY 240
 DB 270 CIVSMLTRKFLY 280
 RESULT 5
 0935ND5 PRELIMINARY; PRT; 277 AA.
 AC 0935ND5;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Caspase-3.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NC NCBI_TaxId=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21334413; PubMed=11440638;
 RA Muneta Y., Shimajima Y., Mori Y.,
 RT "Porcine caspase-3: cloning and its activity during apoptosis of
 RT porcine PK15 cells induced by porcine Fas-1lgand.";
 RL J. Interferon Cytokine Res. 21:409-415(2001).
 DR EMBL; AB029345; BAB5544.1; --.
 DR MEROPS; C14.003; --.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR Pfam; PF00655; ICE_p10; 1.
 DR Pfam; PF00656; ICE_p20; 1.
 DR PROSITE; PS01122; CASPASE_CYS; UNKNOWN_1.
 DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 SQ SEQUENCE 277 AA; 31379 MW; 616C0F56141B012B CRC64;

Query Match 22.2%; Score 274.5; DB 6; Length 277;
 Best Local Similarity 37.3%; Pred. No. 2.8e-15;
 Matches 82; Conservative 27; Mismatches 94; Indels 17; Gaps 8;

QY 29 REGSEDLALHEMFRLRFEFTMKRDPDTAEQFOEELKFOAIDSREDPVSCAFVYLM 88
 DB 64 RSGTDVDAANLREFTNLTKEVRNKNLDTREIELMHSVSKEDHSRSPIC---VLIS 120
 QY 89 HGREGLKGEDEGMVKTENLFEALNNKQALRAKPKVYIIACRGEGRDPG-ETVGGDE 147
 DB 121 HGEGLKIFGTNGP-VDLKKTLSFFRGDCRRTLTGKPKLFIIOACRGTELDGIFTDSCTE 179
 QY 148 IVMYIKDSPTPIPTVDALHYSTVEGVYIAVRHDKGSCFIQTLDVFTKRGHILEL-- 205
 DB 180 DDMAC---QKTPVADFLVYSTAPGYSWRNKSQSWFIQSLCAAL-KOYVAKLELMH 234
 QY 206 -LLEVTNRMA-EAELVQEGK---ARKTNPEIQSTLRKRLY 240
 DB 235 ILTRVNRKVNVEFESFSTDSFHAKKQIPCLVSMLTRKFLY 274

RESULT 6
 0919L7 PRELIMINARY; PRT; 383 AA.
 AC 0919L7;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Caspase.
 GN CASPY.
 OS Brachydanio rerio (zebrafish) (zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Oetartiopterygii; Cypriniformes;
 OC Cyprinidae; Danio.
 NC NCBI_TaxId=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20373792; PubMed=10917738;
 RA Inohara N., Nunez G.,
 RT "Genes with homology to mammalian apoptosis regulators identified in
 RT zebrafish.";
 RL Cell Death Differ. 7:509-510(2000).
 DR EMBL; AF233434; AAF66364.1; --.
 DR HSSP; P29466; ICE.
 DR InterPro; IPR002398; ICE.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR InterPro; IPR004020; PAAD_DAPIN_dom.
 DR Pfam; PF00655; ICE_p10; 1.
 DR Pfam; PF00656; ICE_p20; 1.
 DR Pfam; PF02758; PAAD_DAPIN; 1.
 DR PRINTS; PR00376; ILIBENZYM.

DR SMART, SM00115; CASC: 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 SO SEQUENCE 383 AA; 43966 MW; 21890871309774C3 CRC64;

Query Match 22.2%; Score 274.5; DB 13; Length 383;
 Best Local Similarity 30.0%; Pred. No. 4.2e-15;
 Matches 69; Conservative 49; Mismatches 83; Indels 29; Gaps 6;

QY 29 REGSEEDLALHMRQLRFESTMKRDPFAEQFQELFKFOAIDSRDPVSCAFVYMA 88
 DB 162 RGSSEKDEENMEKLKELDYQVAKRPNLSAKEDFAIRPFAQREBKYS--DSAFVYMS 219

QY 89 HGREGFLKG-----EDGEWVKLENLFEALNNKNCOALRAKPKVYIIQACRGEOR---- 137
 DB 220 HKKRALMKVHYHRTNPSPDSFPVDVYRRLNSENCPALRDKPKVILLIACRGSGRW 279

QY 138 ---DPGETVGDEIVMVIKDSPTQIPIFYTDALHYSTVEGYIAYRHDKSCFIQTIVD 193
 DB 280 ASDGPDEIEIEDDDFVHKEK-----DFISLMSCTPDTKSYHYHNGTFYVQTIVD 331

QY 194 VFTK--RKGHILELLEVTERRMAEALVQEGARKTNPEIQSTLRKRLYL 241
 DB 332 VFICKAHEDHIEELFRKVLRRFHPNMI--GNFKQWACKDRATLPFLFYL 379

RESULT 7

Q9QW14 PRELIMINARY; PRT; 220 AA.

AC Q9QW14; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE CPP32 apoptotic protease (Fragment).
 GN CASP3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Denis F., Alam A., Cohen L., Hartgers F., Braun M., Martinez O.,
 RA Fortin J.-P., Sekaly R.-P.;
 RT "Multiple Pathways of Apoptosis Converging on the CPP32 Protease."
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63720; AAC09504.1; -.
 DR HSSP; P42574; IPAU.
 DR MEROPS; C14.003; -.
 DR MGD; MGI:107739; Casp3.
 DR InterPro; IPR002398; ICE.
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR Pfam; PF00655; ICE_P10; 1.
 DR Pfam; PF00656; ICE_P20; 1.
 DR PRINTS; PR00376; IL1BCENZYM.
 DR SMART; SM00115; CASC: 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 KW Protease.
 FT NON TER
 SQ SEQUENCE 220 AA; 25050 MW; FE7F4857C4EBA544 CRC64;

Query Match 22.1%; Score 273.5; DB 11; Length 220;
 Best Local Similarity 34.1%; Pred. No. 2.6e-15;
 Matches 75; Conservative 34; Mismatches 96; Indels 15; Gaps 6;

QY 28 AREGSEEDLALHMRQLRFESTMKRDPFAEQFQELFKFOAIDSRDPVSCAFVYMA 87
 DB 6 AANGTDVDAANLRETFMGKLYQVRNKNDLTREIDILMLDSVSKEDHSKRSFVC--VIL 62

QY 88 AHGREGFLKGEDENWVKLENLFEALNNKNCOALRAKPKVYIIQACRGEORPG-ETVGD 146
 DB 63 SHGDGVLYGTNGP-VELKKLITSPFRGDCRSLTGKPLFIQACRGELDCGIETDGT 121

QY 147 EIVMVIKDSPTQIPIFYTDALHYSTVEGYIAYRHDKSCFIQTIVDFT--KRGHILE 204
 DB 122 DEEMAC---OKIPYEAFLVAYSTAPGYYSWRNSKDSWFIQSLCMLKYAHKLQFMH 177

QY 205 ILTEVTRRMA---EALVQEGARKTNPEIQSTLRKRLYL 240
 DB 178 ILTRVNRKVATEFESFSDSTFHAKKQFCIVSMILTKELY 217

RESULT 8

Q96AN1 PRELIMINARY; PRT; 277 AA.

AC Q96AN1; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical 31.6 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC016926; AAH16926.1; -.
 DR InterPro; IPR002398; ICE.
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR Pfam; PF00655; ICE_P10; 1.
 DR Pfam; PF00656; ICE_P20; 1.
 DR PRINTS; PR00376; IL1BCENZYM.
 DR PROSITE; PS01122; CASPASE_CYS; UNKNOWN 1.
 DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 277 AA; 31608 MW; 2F35CD3BCF7FE64A CRC64;

Query Match 22.1%; Score 273.5; DB 4; Length 277;
 Best Local Similarity 31.9%; Pred. No. 3.4e-15;
 Matches 80; Conservative 39; Mismatches 103; Indels 29; Gaps 9;

QY 9 EEKYMSGALALILCVTK-----AREGSEEDLALHMRQLRFESTMKRDPFA 58

DB 34 DNSYKMDYPMGLCIIINNKNPHKSTGWTSGTGVDAAANLRETFRNLYEVRNKNNDLTR 93

QY 59 EFOFQELFKFOAIDSRDPVSCAFVYMAHGRBGLKGEDG--EMVKLENLFEALNNKN 116
 DB 94 EEIVELMRDVSKEKSDHSKRSFVC--VILSHGEEGIIIFGTNGPVDLKKITNFF--RGDR 147

QY 117 COALRAKPKVYIIQACRGEORPG-ETVGDGVIVVINDSPQITFYTDALHYSTVEGY 175
 DB 148 CSSLTGKPKLFIQACRGELDCGIETDSGVDDDAC---HKILVEADFLVASTAGY 203

QY 176 IAYRHDKSCFIQTIVDVFVK--RKGHILELLEVTERRMA-EALVQ---EGARKTNP 229
 DB 204 YSMRNSKDSWFIQSLCMLKQYADKLEFMIHLTTRVNRKVATEFESFSDATFHAKKQIP 263

QY 230 EIOSTLRKRLYL 240

DB 264 CIVSMILTKELY 274

RESULT 9

Q9IB63 PRELIMINARY; PRT; 399 AA.

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AC Q91B61;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Caspase-9.
GN XCAPSPASE-9.
OC Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
OX NCBI_TaxID=8355;
RN
RP SEQUENCE FROM N.A.
RA MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yaeita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
RT family."
RL J. Biol. Chem. 275:10484-10491 (2000).
DR EMBL; AB038172; BAA94750.1; -.
DR HSSP; Q15806; 1QDU.
DR MEROPS; C14.010; -.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR000488; Death.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00655; ICE_p10; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PRINTS; PR00376; ILBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
SQ SEQUENCE 399 AA; 44772 MW; EE2A269719064F9F CRC64;

Query Match 22.0%; Score 272; DB 13; Length 399;
Best Local Similarity 27.9%; Pred. No. 7.1e-15;
Matches 80; Conservative 40; Mismatches 107; Indels 60; Gaps 8;

QY 2 SNRSLSEERK-YDMSGALALILCVT-----KAREGEEDLDALBEMFROLRFES 50
DB 125 SRKGTLDKXDYPMSSDPICGLIINNMNPHCTGLSTRGSDIDRDKLANRMSFFFEV 184
QY 51 TMRKDPYAEQFOEELKFOQALDSREDPVSCAFVILMAHGRE-----GFLKGEDEMV 103
DB 185 TVKDNLTGQAMHDLQALADQDHSLOD---CCLVVIILSHGCEETHIQPGGVGTGDIRI 241
QY 104 KLENLFEALNNKQNALRAKPKVYIIQACRGEDRPBETVG----- 145
DB 242 PVEKIVSYFNGSKPSPILRGPKFIPIQACGDDQCKCEVSETPPLSPSTSLQSDATP 301
QY 146 -----DEIVWYIKSPQTIPTPTALHYSTVEGYIARHDQKSCFIQTLVDVFTK 197
DB 302 VFSGEGRDV-----DAVSNIPFSDILVSYSTFPFGVSRMDGHTGSMWYEVLDVSLAE 356
QY 198 RKG-HILELLTEVTRMAEALVQESGAKRTNPEIQSTLRKRLYLQ 242
DB 357 HAADLDQSLVWV-----ADGVSSKGTQYQIPGVFNFLKRFYFK 397

RESULT 10
Q96KP2 PRELIMINARY; PRT; 277 AA.
AC Q96KP2;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Caspase-3.

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GN CASP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN
RP SEQUENCE FROM N.A.
RA Vallente F.M.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Oliver L.J.;
RT "Control of the activation of the procaspase-3 by a sequence located
RT at the N-terminus of the p17 subunit."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; A413269; CAC08866.1; -.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00655; ICE_p10; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PRINTS; PR00376; ILBENZYM.
DR PROSITE; PS01122; CASPASE_CYS; UNKNOWN_1.
DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 277 AA; 31642 MW; 6162767B0D2DE021 CRC64;

Query Match 21.8%; Score 270.5; DB 4; Length 277;
Best Local Similarity 34.7%; Pred. No. 6.1e-15;
Matches 77; Conservative 35; Mismatches 91; Indels 19; Gaps 8;

QY 28 ARGESEEDLDALBEMFROLRFESTMGRDPTAEQFOEELKFOQALDSREDPVSCAFVLM 87
DB 63 SRGTVDANLNETRNKLKYEVRANKDLTREIVELMRVSEKDSKSSFCV--VLL 119
QY 88 AHGREGEFLKGEDG--EMVKLENLFEALNNKQNALRAKPKVYIIQACRGEDRPB-ETVG 144
DB 120 SHGEGEIIFFCTNGPVDLKITTF--RGDRCSRLTGKPKPLFIQACRGTELDGIEITDS 176
QY 145 GDEIVWYIKSPQTIPTPTALHYSTVEGYIARHDQKSCFIQTLVDVFTK--RKGHI 202
DB 177 GVVDDMAC---HKIPDADFVLYASTAPGYSMRNSKDSWFIQSLCAMLKQYADLIER 232
QY 203 LEDTEVTRMA-EAEVLQ---EGKARKTNPEIQSTLRKRLY 240
DB 233 MHILTRVNRKVATEFESFSDATFPAKQIPLCIIVSLTKELY 274

RESULT 11
Q98550 PRELIMINARY; PRT; 303 AA.
AC Q98550;
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Caspase-7.
GN Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN
RP SEQUENCE FROM N.A.
RA TISSUE=SPLEEN.
RC
RA Forghani F., Roy S.;
RT "Rat caspase-7 sequence."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF072124; AAC24011.1; -.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.004; -.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.

```

DR Pfam: PF00655; ICE_p10; 1.
 DR Pfam: PF00656; ICE_p20; 1.
 DR PRINTS; PR00376; ILIBCNZYME.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_p10; 1.
 DR PROSITE; PS50208; CASPASE_p20; 1.
 SQ SEQUENCE 303 AA; 34324 MW; A11728754BF199DD CRC64;

Query Match 21.8%; Score 270; DB 11; Length 303;
 Best Local Similarity 32.6%; Pred. No. 7, 5e-15;
 Matches 71; Conservative 36; Mismatches 101; Indels 10; Gaps 4;

QY 29 REGSEEDLDALHMFROLRFESTMKRDPFAEQFOELEKFOQAIDSREDPVSCAFVLA 88
 DB 87 RRGDCKDAEALFKCRSLGFEVTVYVNDSCAMQDLRLRASEEDHSN---ACFACVLIS 143
 QY 89 HGREGFLKGEDEGMVKLENLFEALNNKNCQALRAKPKVYIIQACRGQRDPGETVGDEI 148
 DB 144 HGEENLITGKDG-VTPIKDLTAHFGRDKTLLEKPLFFIACRGTELDSDIGQADSGFI 202
 QY 149 VVWIKDSPQITPTYTDAHVSTVEGYIAYRHQDGSCFIQTLDVFTK--RKGHILELL 206
 DB 203 NDTANPRKIPVEADFLFAYSTVPGYYSWRNPGKSGMFWQALCSILNHHGDLIMQIL 262
 QY 207 TEVTRMAEALVOEGKAR---KTNPEIQSTLRKRLY 240
 DB 263 TRVNDVARHFSQSDDPFRFNEKQIPCMVSMILYELY 300

RESULT 12

Q9ROT0 PRELIMINARY; PRT; 454 AA.
 ID Q9ROT0;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Caspase9.
 GN CASP9.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20001956; Pubmed=10529400;
 RA Fujita E., Jimbo A., Matuzaki H., Konishi H., Kikawa U., Momoi T.;
 RT "Akt phosphorylation site found in human caspase-9 is absent in mouse
 caspase-9";
 RL Biochem. Biophys. Res. Commun. 264:550-555(1999).
 DR EMBL; AB019600; BAA86895.1; -.
 DR HSSP; P42574; 1PAU.
 DR MEROPS; C14.010; -.
 DR MGD; MGI:1277950; Casp9.
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR002398; ICE.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00655; ICE_p10; 1.
 DR Pfam; PF00656; ICE_p20; 1.
 DR PRINTS; PR00376; ILIBCNZYME.
 DR SMART; SM00114; CARD; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_p10; 1.
 DR PROSITE; PS50208; CASPASE_p20; 1.
 SQ SEQUENCE 454 AA; 50051 MW; 4614989AFe823850F CRC64;

Query Match 21.8%; Score 269.5; DB 11; Length 454;

Best Local Similarity 30.6%; Pred. No. 1, 4e-14;
 Matches 76; Conservative 37; Mismatches 88; Indels 47; Gaps 7;

QY 29 REGSEEDLDALHMFROLRFESTMKRDPFAEQ---FOELEKFOQAIDSREDPVSCAFV 84
 DB 218 RTGNNLRDKLEHFRFWREVEYKNDLTAKQVYALMAHNRHRLD-----CFVV 270
 QY 85 VLMAGRE-----GFLKGEDEGMVKLENLFEALNNKNCQALRAKPKVYIIQACRGQR 137
 DB 271 VILSHGQASHLQFPNAVYGTGDCSVSIEKLVNFNSGSGCPISLGRKPLFIQACGGEQK 330
 QY 138 D-----PGETVGDEIWMVIK-----DSPQITPTYTDAHVSTVEGYI 176
 DB 331 DHGEVACTSSQGRITLDSSEPDAPVYQEGRPPLDOLDAVSLPTPSDILVYSTPFGFV 390
 QY 177 AYRHQDGSCFIQTLDVFTK--RKGHILELLTEVTRMAEALVOEGKARKTNPEIOST 234
 DB 391 SWRDKSGSWYIEITLDGILEQWARSDELQSLLRV-----ANAVSEKGYTKQIPGCENF 444
 QY 235 LRKRLYIQ 242
 DB 445 LRKRLFFK 452

RESULT 13

Q90WU1 PRELIMINARY; PRT; 482 AA.
 ID Q90WU1;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Caspase 8.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Barton S., Bridgham J.T., Johnson A.L.;
 RT "Caspase-8 and -9 expression in the hen ovary";
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY057939; AAL23700.1; -.
 DR InterPro; IPR001875; DED.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR Pfam; PF01335; DED; 2.
 DR Pfam; PF00655; ICE_p10; 1.
 DR Pfam; PF00656; ICE_p20; 1.
 DR PROSITE; PS01122; CASPASE_CYS; UNKNOWN_1.
 DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
 DR PROSITE; PS50207; CASPASE_p10; 1.
 DR PROSITE; PS50208; CASPASE_p20; 1.
 DR PROSITE; PS50168; DED; 2.
 SQ SEQUENCE 482 AA; 54645 MW; 8E3936BEE090BEF CRC64;

Query Match 21.7%; Score 269; DB 13; Length 482;
 Best Local Similarity 29.7%; Pred. No. 1, 6e-14;
 Matches 66; Conservative 50; Mismatches 92; Indels 14; Gaps 5;

QY 27 KARESEEDLDALHMFROLRFESTMKRDPFAEQFOELEKFOQAIDSREDPVSCAFVLA 86
 DB 261 KRRNGTHVDADLRLKRVFSNLHTVAEYDCDTELRINLVNVRCHDHNNK---CFVCCI 317
 QY 87 MAHGREGLKGEDEGMVKLENLFEALNNKNCQALRAKPKVYIIQACRGQRDPG---ETV 143
 DB 318 LSHGKDDIYGVDCQGEVPIQIELTTSFTGQNCQSLGAKRKVFVQACQGDAYQKGVYIETD 377
 QY 144 GGDVLMVTKDSP---QITPTYTDAHVSTVEGYIAYRHQDGSCFIQTL---VDVFTK 197
 DB 378 SGEQVYSLETDAFQDLDCIPSEADFLGNTTLDQDVSVSPSQGWYIQLSCQHLSSCP 437
 QY 198 RKGHILELLTEVTRMAEALVOEGKARKTNPEIOSTLRKRL 239

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 26, 2003, 12:17:35 ; Search time 26.5139 Seconds
(without alignments)
877.445 Million cell updates/sec

Title: US-09-989-903-5

Perfect score: 1239

Sequence: 1 MSNPRSLSEEEKYDMSGALAL.....KARKTNPETQSTLRKRLYLQ 242

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1234	99.6	242	2 JC7517	caspace-14/a - hum
2	293	23.6	452	2 JC6507	caspace-2 - rat
3	289	23.3	435	2 A54821	apoptosis regulato
4	282.5	22.8	277	2 JC5410	CPB32 protein - mo
5	280.5	22.6	277	2 S64710	cysteine proteinas
6	272.5	22.0	277	2 A55315	cysteine proteinas
7	264.5	21.3	454	2 JC7123	caspace-9 long cha
8	248.5	20.1	503	2 A49429	interleukin-1 beta
9	246.5	19.9	212	2 I67437	cysteine proteinas
10	239.5	19.3	416	2 G02635	ICE-LAP6 - human
11	230	18.6	495	2 T20038	hypothetical prote
12	226	18.2	311	2 B56084	interleukin-1beta
13	226	18.2	383	2 A56084	interleukin-1beta
14	226	18.2	404	2 A42677	interleukin-1 beta
15	225	18.2	418	2 B57511	interleukin-1 beta
16	217.5	17.6	402	2 A46495	IL-1 beta converta
17	213.5	17.2	482	2 I67436	interleukin-1-beta
18	210.5	17.0	826	2 T43638	caspace-related pr
19	207	16.7	263	2 C56084	interleukin-1beta
20	205.5	16.6	377	2 A57511	interleukin-1 beta
21	197	15.9	312	2 B54821	apoptosis regulato
22	189	15.3	536	2 T43633	caspace-related pr
23	185	14.9	488	2 T13385	hypothetical prote
24	174.5	14.1	642	2 T27021	hypothetical prote
25	159.5	12.9	136	2 I53300	interleukin-1-beta
26	103.5	8.4	1313	2 A48467	myosin heavy chain
27	98	7.9	1957	2 A45627	myosin heavy chain
28	97.5	7.9	139	2 T43642	caspace protein 3
29	97	7.8	1051	2 T18302	apB protein - Eme

30	95.5	7.7	1190	2 E84193	chromosome segrega
31	95.5	7.7	2104	2 T38774	myosin-3 heavy cha
32	95	7.7	761	2 E82205	chemotaxis protein
33	91	7.3	394	2 T26968	hypothetical prote
34	91	7.3	510	2 S42626	BR-golgi intermedi
35	90.5	7.3	520	2 F70350	recombination prot
36	89.5	7.2	467	2 D95253	L-fuculose kinase
37	89.5	7.2	482	2 B98118	thamulokinase (EC
38	89.5	7.2	1225	2 A56514	chromokinesin - ch
39	89	7.2	352	2 G71328	probable flagellar
40	88.5	7.1	149	2 T43637	caspace protein 1C
41	88.5	7.1	661	2 B97733	excinuclease ABC s
42	88.5	7.1	858	1 IJRTNC	neural cell adhesi
43	88.5	7.1	1203	2 B55094	chromosomal protei
44	88.5	7.1	2954	2 T14156	kinasin-related pr
45	88	7.1	505	2 S39520	H+-transporting tw

ALIGNMENTS

RESULT 1
JC7517
caspace-14/a - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C/Accession: JC7517
R/Eckhart, L.; Ban, J.; Fischer, H.; Tschachler, E.
Biochem. Biophys. Res. Commun. 277, 655-659, 2000
A/Title: Caspace-14: Analysis of gene structure and mRNA expression during keratinocyte
A/Reference number: JC7517; MUID:20517231; PMID:11062009
A/Contents: Epidermal keratinocytes
A/Accession: JC7517
A/Molecule type: mRNA
A/Residues: 1-242 <ECK>
A/Cross-references: GB:AF097874
C/Comment: This enzyme accumulates during keratinocyte differentiation and is activated
C/Genetics:
A/Map position: 19p13.1
A/Introns: 9/3; 59/3; 135/1; 174/1; 208/3
C/Keywords: differentiation

Query Match 99.6%; Score 1234; DB 2; Length 242;
Best Local Similarity 99.6%; Pred. No. 1.1e-88;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLDALBHMFRQLRPSTMKDPTAEQ 60
Db 1 MSNPRSLSEEEKYDMSGARLALILCVTKAREGSEEDLDALBHMFRQLRPSTMKDPTAEQ 60
QY 61 FOELEKFOQALIDREDPVSCAFVLMAGREGFLKEDGEMVLEULFEALNNKNCAL 120
Db 61 FOELEKFOQALIDREDPVSCAFVLMAGREGFLKEDGEMVLEULFEALNNKNCAL 120
QY 121 RAKKRVYIIQACRGEOBPPGETVSGDEIVMWYIKDSPOTIPYTDALHYSTVEGYIAYRH 180
Db 121 RAKKRVYIIQACRGEOBPPGETVSGDEIVMWYIKDSPOTIPYTDALHYSTVEGYIAYRH 180
QY 181 DOKSGCFIQLVDVFTYRKKGHILELTVTRMAEAEIVGKARKTNPETQSTLRKRLY 240
Db 181 DOKSGCFIQLVDVFTYRKKGHILELTVTRMAEAEIVGKARKTNPETQSTLRKRLY 240
QY 241 LQ 242
Db 241 LQ 242
RESULT 2
JC6507
caspace-2 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: J06507
 R:Sato, N.; Milligan, C.E.; Uchiyama, Y.; Oppenheim, R.W.
 Gene 202, 127-132, 1997
 A:Title: Cloning and expression of the cDNA encoding rat caspase-2.
 A:Reference number: J06507; MUID:98087427; PMID:9427555
 A:Accession: J06507
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-452 <SAT>
 A:Cross-references: GB:U77933; NID:92769705; PIDN:AB96379.1; PID:92769706

Query Match 23.6%; Score 293; DB 2; Length 452;
 Best Local Similarity 31.5%; Pred. No. 3e-15;
 Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

Qy 29 RGSSEDDDLAEMHPRQLRFESTMKRDPFAEQFOELERFOQALDSREDPVSCAFVYMA 88
 Db 219 RSGGVDDHTTLVTLFPLGLGVNHLVDQTAQEWQELQNFQAQ-LPAAHVTDSC-IVALLS 276
 Qy 89 HREGFLKGEDEEMVLENTLFEALNNKNCQALRAKPKYIIQACRGEORDPG----- 140
 Db 277 HVEGGIVVDGKLTQLQGVFRLFDNANCPSLONKPKMFIIQCRGDETRGVDDQDGKN 336
 Qy 141 -----ETVGGDEIVMWIKDSPQTIPTTDLAHVYSTEGLIAYRHQKSCFIQTLV 192
 Db 337 HAQSPCCESDAGKEBELMKR-----LPTRSDMICGYACLKGNAAARNTKRGSWYTEALT 391
 Qy 193 DVFTKR--KGHLELLTEVTRMAEALVQEGKARKTN-----PEIOTLRKRLYL 241
 Db 392 QVFSEBAQCMHVAQMLVKVNALIKD---REGVAPGTETFRCKEMSEYSTLCQQLYL 445

RESULT 3

A:Accession: A54821
 A:Title: ICH-1, a stimulatory form L - human
 A:Species: Homo sapiens (man)
 C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
 C:Accession: A54821
 R:Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
 Cell 78, 739-750, 1994
 A:Title: ICH-1, an IGF-1-related gene, encodes both positive and negative regulators
 A:Reference number: A54821; MUID:94373811; PMID:8087842
 A:Accession: A54821
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-435 <MAN>
 A:Cross-references: GB:U13021; NID:9537291; PID:9537292
 C:Keywords: alternative splicing; apoptosis

Query Match 23.3%; Score 289; DB 2; Length 435;
 Best Local Similarity 31.1%; Pred. No. 5.8e-15;
 Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

Qy 29 RGSSEDDDLAEMHPRQLRFESTMKRDPFAEQFOELERFOQALDSREDPVSCAFVYMA 88
 Db 202 RSGGVDDHTTLVTLFPLGLGVNHLVDQTAQEWQELQNFQAQ-LPAAHVTDSC-IVALLS 259
 Qy 89 HREGFLKGEDEEMVLENTLFEALNNKNCQALRAKPKYIIQACRGEORDPG----- 140
 Db 260 HVEGGIVVDGKLTQLQGVFRLFDNANCPSLONKPKMFIIQCRGDETRGVDDQDGKN 319
 Qy 141 -----ETVGGDEIVMWIKDSPQTIPTTDLAHVYSTEGLIAYRHQKSCFIQTLV 192
 Db 320 HAQSPCCESDAGKE-----KLPKMRLLPTRSDMICGYACLKGNAAARNTKRGSWYTEALT 374
 Qy 193 DVFTKR--KGHLELLTEVTRMAEALVQEGKARKTN-----PEIOTLRKRLYL 241
 Db 375 QVFSEBAQCMHVAQMLVKVNALIKD---REGVAPGTETFRCKEMSEYSTLCQQLYL 428

RESULT 4
 J05410
 CPP32 protein - mouse

C:Species: Mus musculus (house mouse)
 C:Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999
 C:Accession: J05410
 R:Murakami, T.; Urae, K.; Momoi, M.Y.; Kimura, I.; Momoi, T.
 Biochem. Biophys. Res. Commun. 231, 770-774, 1997
 A:Title: Specific expression of CPP32 in sensory neurons of mouse embryos and activation
 A:Reference number: J05410; MUID:97224429; PMID:9070890
 A:Accession: J05410
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-277 <MKU>
 A:Cross-references: DDBJ:D86352
 A:Experimental source: embryo
 C:Comment: This protein is involved in the apoptosis of dorsal root ganglia neurons.

Query Match 22.8%; Score 282.5; DB 2; Length 277;
 Best Local Similarity 32.4%; Pred. No. 1.1e-14;
 Matches 81; Conservative 38; Mismatches 104; Indels 27; Gaps 8;

Qy 9 BEKYMSGALALILCVT-----KAREGSEDDDLAEMHPRQLRFESTMKRDPFA 58
 Db 34 DSYKMDYPMKICITITNKPFHSTGMSRSGTDVDAANLRFTMGUKYEVKRNKNDLTR 93
 Qy 59 EQFOELERFOQALDSREDPVSCAFVYMAHREGFLKGEDEEMVLENTLFEALNNKNCQ 118
 Db 94 BEIMELMDSVSKEDHSKSSFC---VILSHGDEGVIRGTNGP-VDLKRLTSFFRGDYCR 149
 Qy 119 ALRAKPKYIIQACRGEORDPG-ETVGGDEIVMWIKDSPQTIPTTDLAHVYSTEGLIA 177
 Db 150 SLTGPKPKFIITQACRGTLDGIEITDSGTDEMAC---QKIPEVADPLVYSTAPGYVS 205
 Qy 178 YRHQKSCFIQTLVDVFTKRKHILE--LLEVTRMA-----EAEVQEGKARKTNPE 230
 Db 206 WRNSKDGSMFIQSLQSLML-KLYAHLEFMHILITRNKRVATFEFSFSDSTFHAKQILPC 264
 Qy 221 IOSTLRKRLYL 240
 Db 265 IVSMILTKEYL 274

RESULT 5

S64710
 A:Title: cys21, a cys21 gene (EC 3.4.22.-) CPP32 - Chinese hamster
 A:Species: Cricetus griseus (Chinese hamster)
 C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
 C:Accession: S64710; S72395
 R:Wang, X.; Zelenek, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.
 EMBO J. 15, 1012-1020, 1996
 A:Title: Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 during
 A:Reference number: S64710; MUID:96183185; PMID:8605870
 A:Accession: S64710
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-277 <MAN>
 A:Cross-references: EMBL:U27463
 R:Wang, X.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: S72395
 A:Accession: S72395
 A:Molecule type: mRNA
 A:Residues: 1-79, 'A', '81-146', 'Y', '148-277 <MAN>
 A:Cross-references: EMBL:U27463; NID:91244443; PIDN:AB01511.1; PID:91244444
 C:Keywords: apoptosis; cysteine proteinase; hydrolase

Query Match 22.6%; Score 280.5; DB 2; Length 277;
 Best Local Similarity 35.9%; Pred. No. 1.6e-14;
 Matches 79; Conservative 31; Mismatches 93; Indels 17; Gaps 7;

Qy 29 RGSSEDDDLAEMHPRQLRFESTMKRDPFAEQFOELERFOQALDSREDPVSCAFVYMA 88
 Db 64 RSGTVDAAKRLRETWMNKYEVKRNKDLREIYELMKNAKEDHSKSSFC---VILS 120
 Qy 89 HREGFLKGEDEEMVLENTLFEALNNKNCQALRAKPKYIIQACRGEORDPG-ETVGGDE 147

Db 121 HGDEVIIGTGGP-IDLKKLSTYRGGDCRSLIGPKLFIQAARGVBLDGIETDSGTE 179

Qy 148 IWMVKDSPQTIPIYTDLAHVSTVEGYIAVRHDOKSGCFIQLVDFYTKRGHILE-- 204

Db 180 DDMTC----QKIPVADFLYAVSTAPGYSWRNPDGSMFIQSLCSML-KLYAHKLEFMH 234

Qy 205 LLEVTREMA----EAEVGGGKARKNPQLQSLTKRKLY 240

Db 235 ILTRNRRKVAATEFESFSLDSTFPAKKQIPLCVISMILTELY 274

RESULT 6
A55315

N:Alternate names: cysteine proteinase CPP32
C:Species: Homo sapiens (man)

C/Accession: A55315; S58899; T39005
R; Fernandes-Alnemri, T.; Litwack, G.; Alnemri, E.S.

A1>Title: CPP33, a novel human apoptotic protein with homology to Caenorhabditis elegans
A1.Reference number: A55315, MUID:95074098, PMID:7983002

A:Status: preliminary
A:Molecule type: mRNA

A: Cross-References: GB:U13737, NID:9561665, PIDN:AA65015.1, PID:9561666
R: Nicholson, D.W.; Alt, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant,

A:Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammalian

A:Accession: S58899
A:Molecule type: protein

R.Tewari, M.; Quan, L.T.; O'Rourke, K.; Denoyers, S.; Zeng, Z.; Beidler, D.R.; Poirier
Cell 81, 801-809, 1995

A:Accession: I39005
 A:Reference number: A56924; MWID:95292347; PMID:7774019
 A:Access: 2000/01/22 local; 4 intermediate homologs of CUB-5; 15 a CUB-110010406 place388

A;Residues: 1-189, 'E', 191-277 <RES>
A;Molecule type: mRNA
A;Status: predictedly

Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

Query match	22.0%	Score 2/2.5	DB 2	Length 211
Best Local Similarity	31.9%	Pred. No. 6:5e-14;		
Matches 80: Conservative	39:	Mismatches 103:	Indels 29:	Gaps 9:

```
0Y      9 EEKYDMSGALALLICVTK-----AREGSSEEDLDALHEHFRQLRPESTMKDPPTA 58
```

59 E0F0EELEKFO0A1DSREDPVSCAEVYLMAHGREGFLKGGNG--EMVKLENI.PEAT.NNKN 116

```
Db      94 EEIVELMDVSKEDHRSRSPVC---VLISHGEGIIFGTNGPVDLKITNPF--RGDR 147
```

DB 148 CRSLTGKPKLFTTQACRGTEFLDCGIFETSDGVDNDMAC-----HKLPVDNDEL VYSTTBGV 203

DY 176 IAYHDKGSCFIQTLVDVFVK--RKGIILELLTEVTRRMK-EAEVLQ---EGSKARTNP 229
:: :: : ||| |

05 230 E10ST1ARKB1.Y 240
06 204 Y5WNR5K0G5WF1Q5LCLCMLKQYADUKLEFPHLITRVRKRVATBESFSFDATEFHAQQIP 263

Db 264 CIVSMILTKELY 274

RESULT 7

caspase-9 long chain - mouse
JC7123
C.Species: Mus musculus (house mouse)
C.Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C.Accession: JC7123
R.Fujita, E.; Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikawa, U.; Momoi, T.
Biochem. Biophys. Res. Commun. 264, 550-555, 1999
Article: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9
A.Reference number: JC7123; MUID:20001956; PMID:10529400

A;Residues: 1-454 <FUJ>
A;Cross-references: DDBJ:AB019600; NID:g6440941; PID:g6440942

Query Match	21.3%	Score 264.5;	DB 2;	Length 454;
Best Local Similarity	30.6%	Pred. NO. 4.9e-13;		

QY 29 REGSEEDIDALEHMFRLRFESTMKRDPTEQ----FQSELEKFKQQAIDSRDEPVSCAFV 84

Db 218 RTGSNIDRDKLEHRFRWLRFMEVKNDLTAKKNTALMEMAHRHRAID-----CPVV 270

Db 271 VIIISHGCCASHLOFGAYVYGTDCGVSIEIKIVINFGNSCCPSLGGPKPLFFIQACGGEQK 330

Qy 138 D-----PGETVGDGEIWNVIK-----DSPQTITPTYTDLHVSTVEGNI 176
| : | : : : : : : : : : : : :
| : : : : : : : : : : : :

177 AYRHDKSCFIOTLVNFTK--RKGHILELLEVTNRMAEAEIVQEGARKTNPEIOGT 234

Db 391 SWDDKSSGWSYIETLDGILFQWARSEDIQSLLRV-----AAAVSEKGYKQIPGCFNF 444

27	222		212
Db	445	LRRKLFFK	452

RESULT 8

A43429
interleukin-1 beta-converting enzyme homolog CSD-3 -
Caenorhabditis elegans
C:Species: Caenorhabditis elegans

R:Yuan, J.; Shiham, S.; Iedoux, S.; Ellis, H.M.; Horvitz, H.R.
C:Patte: 07-APR-1994 #sequence_leviation 18-NOV-1994 #excl_change 01-DEC-2000
C:Accession: A49429; T37312

A:Reference number: A49429; MUID:94061982; PMID:8242740
A:title: The C. elegans cell death gene ced-3 encodes a protein similar to mammal cell /5, 641-652, 1993

A:accession: A49429
A:Status: preliminary
A:Molecule type: DNA

A:Note: sequence extracted from NCBI backbone (NCBITN:139825 NCBITP:139826)
A:Cross-references: GB:U29052; NID:g6503232; PIDN:AAA27982.2; PID:g6503233
A:Residues: 1-503 <YUA>
A:Residues: 1-503 <YUA>

A;Accession: T37312
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA

A;Residues: 1-417, 'R', 419-503 <YU2>
A;Cross-references: EMBL: L29052; PIDN: AAA27982.1
C;Genetics:

A;gene: ced-3
A;introns: 45/3; 94/2; 179/1; 289/3; 361/1; 403/3; 483/3

Query Match	20.1%	Score 248.5	DB 2	Length 503
Best Local Similarity	27.9%	Pred. No. 9.7e-12		
Matches 68: Conservative	42	Mismatches 93	Indels 41	Gaps 6

QY 29 RESEEDIDALEHMFROLPFESTMKRDPPTAEOFOEELEKFOAIDSREDPVSCAFVILMA 88

D5 259 RINGKADKDNLTNLFRCMGYTVICKDNLTCGRGMLTTIRDFAK----HESHGDSALVILIS 314

QY 89 HGREGLKGEDEEMVKNLELFEALNNKCOALRAKPKYIIQACRGQRDPGEV----- 143
 DB 315 HGEENVIIIGVDIPISTHEIYDLNNAANPRLANPKYIVFQACGERDNGFPVLDSVD 374
 QY 144 -----GGDEIVNVIKDSP-----QTIPTFDALHVSSTVEGYIAYR 179
 DB 375 GVPAPFLRRGMDN-----RDGPLFNFPLGCVRPQVOQVWRKPSQADILIAVATTAQYVSWR 429
 QY 160 HDQKSGCFIQTLDVFT--KRGHILTEITRMAEALVQEG--KAKTNPETIOSTLR 236
 DB 430 NSARSGSWFIQAVCEVSTHAKMDVVELTEVKKVACGFQTSQGSNIIKQMPMTSRL 489
 QY 237 KRLY 240
 DB 490 KKFY 493
 RESULT 9
 167437
 Cysteine proteinase (EC 3.4.22.-) P32 - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
 C:Accession: 167437
 R:Flaws, J.A.; Kugu, K.; Tribovich, A.M.; Desanti, A.; Tilly, K.I.; Hirschfield, A.N.; Tili
 Endocrinology 136, 5042-5053, 1995
 A>Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cel
 nulo cells of the ovarian follicle.
 A:Reference number: 153300; M01D:96042508; PMID:7588240
 A:Accession: 167437
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <RES>
 A:Cross-references: EMBL:U34685; NID:g1004370; PIDN:AAC52261.1; PID:g1004371
 C:Keywords: cysteine proteinase; hydrolase
 Query Match 19.9%; Score 246.5; DB 2; Length 212;
 Best Local Similarity 31.5%; Pred. No. 4.9e-12;
 Matches 69; Conservative 34; Mismatches 89; Indels 27; Gaps 8;

QY 9 EKKYDMSGALLLILCVT-----KARSGEDLDALEHMFQALFESTMKRDPFA 58
 DB 5 DSSYKNDYEMGLICIIINKNFHKSTGMSRNGTVDANLETFVALKYEVANKNKDLTR 64
 QY 59 EFOEELERFOOALDSRDPVSCAFVYVMAHGREGLKGEDEEMVKNLELFEALNNKCO 118
 DB 65 EIMELMDSVSKEDSHKSSPVC---VILSHGDEVIPTGNP-VLKLKTSFFRDPYCR 120
 QY 119 ALRAKPKYIIQACRGQRDPG-ETVGG--DEIVNVIKDSPQTIPTFDALHVSSTVEGY 175
 DB 121 SLTGKPKLFIQACRGTELDSGIETSDGADDDVAC-----QKKPEADPLVAYSAPGY 174
 QY 176 IAYRHQKSGCFIQTLDVFTKRGHILE---LITEVTR 211
 DB 175 YSMRNSRSGSWFIQSLC-AMELKLYAHKLEFPMHILTRVNR 212

RESULT 10
 G02635
 ICE-LAP6 - human
 C:Species: Homo sapiens (man)
 C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
 C:Accession: G02635
 R:Dean, H.; Orth, K.; Chinnaiyan, A.M.; Poirier, G.G.; Froelich, C.J.; He, W.W.; Dixit,
 submitted to the EMBL Data Library, April 1996
 A:Reference number: H01513
 A:Accession: G02635
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-416 <DUA>
 A:Cross-references: EMBL:U56390; NID:g1336026; PIDN:AAC50640.1; PID:g1336027
 Query Match 19.3%; Score 239.5; DB 2; Length 416;
 Best Local Similarity 28.7%; Pred. No. 3.9e-11;

Matches 72; Conservative 46; Mismatches 84; Indels 49; Gaps 9;
 QY 27 KARSGEDLDALEHMFQALFESTMKRDPFAOFOEELERFOOALDSRDPVSCAFV 84
 DB 178 RTRGSSNIDCEKLRRRRFSLSHFMEVVKDILTKKMYLALLEL-----ARQHGALDCCV 232
 QY 85 VJMAHGRE-----GFLKGEDEEMVKNLELFEALNNKCOALRAKPKYIIQACRGQR 137
 DB 233 VILSHGCCASHLQFPFGAYVGDGCVSVKIVNIFNGTSCPSLGGKPLFIQACGGEQK 292
 QY 138 DPG-----ETVGG-----DEIVNVIKDSPQTIPTFDALHVSST 171
 DB 293 DHGFEVASTSPEDSPGSPNPDPATPQEGLRTPDQ-----DAISLPTSPSDIFVYST 347
 QY 172 VEGYIAYRHQKSGCFIQTLDVFTKRGHILELITEVTRMAEALVQEGKAKTNPETI 231
 DB 348 PFGFVSMRDPKSGSWYVETLDDIF-EQWAH-SEDLQSLILRVANAVSVK--GIYKQMPGC 403
 QY 232 OSTLRKRLYLQ 242
 DB 404 FNFRLKKLFFK 414

RESULT 11
 120038
 Hypothetical protein C48D1.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: 120038
 R:Burton, J.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: Z19214
 A:Accession: 120038
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-495 <WIL>
 A:Cross-references: EMBL:Z81049; PIDN:CAB02848.1; GSPDB:GN00022; CESP:C48D1.2
 A:Experimental source: clone C48D1
 C:Genetics:
 A:Gene: CESP:C48D1.2
 A:Map position: 4
 A:Introns: 44/3; 93/2; 178/1; 288/3; 360/1; 402/3; 466/1

Query Match 18.6%; Score 230; DB 2; Length 495;
 Best Local Similarity 27.6%; Pred. No. 2.6e-10;
 Matches 60; Conservative 39; Mismatches 78; Indels 40; Gaps 5;
 QY 29 REGSEEDLDALEHMFQALFESTMKRDPFAOFOEELERFOOALDSRDPVSCAFV 88
 DB 258 RNGTRADKDNLTNLPFCMGYTVICKDNLTGRGMLTTIRDPFK---HSHGDSAILVILS 313
 QY 89 HGREGLKGEDEEMVKNLELFEALNNKCOALRAKPKYIIQACRGQRDPGEV----- 143
 DB 314 HGEENVIIIGVDIPISTHEIYDLNNAANPRLANPKYIVFQACGERDNGFPVLDSVD 373
 QY 144 -----GGDEIVNVIKDSP-----QTIPTFDALHVSSTVEGYIAYR 179
 DB 374 GVPAPFLRRGMDN-----RDGPLFNFPLGCVRPQVOQVWRKPSQADILIAVATTAQYVSWR 428
 QY 180 HDQKSGCFIQTLDVFT--KRGHILTEITRMAEALVQEG--KAKTNPETIOSTLR 214
 DB 429 NSARSGSWFIQAVCEVSTHAKMDVVELTEVKKVACGFQTSQGSNIIKQMPMTSRL 465

RESULT 12
 B56084
 Interleukin-1beta converting enzyme gamma isozyne - human
 C:Species: Homo sapiens (man)
 C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
 C:Accession: B56084
 R:Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.
 J. Biol. Chem. 270, 4312-4317, 1995
 A>Title: Cloning and expression of four novel isoforms of human interleukin-1beta conver

A:Reference number: A56084; MUID:95181414; PMID:7876192
 A:Accession: B56084
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-311 <ALN>
 A:Cross-references: GB:U13698; NID:g717041; PIDN:AAC50108.1; PID:g717042
 C:Genetics:
 A:Gene: IL1BC
 C:Keywords: alternative splicing

Query Match 18.2%; Score 226; DB 2; Length 311;
 Best Local Similarity 29.5%; Pred. No. 3.1e-10;
 Matches 77; Conservative 41; Mismatches 89; Indels 54; Gaps 12;

15 SGALALILCVTK-----AREGSEEDLDALHEMFRLRFESTMKRDPFAEQFOEELKFKQ 69
 Db SRTLALILICNEEFDSPRRTGAEDVDITGTMMLQNLGSDVAKNLTASDMTELEAF 126
 QY 70 QAISREDPVSCAFVLMANG-REGFLKGEDEGV-----KLENLFEALNNKNCALRAKP 124
 Db 127 HRPEHKTS--DSTFLVFMHSGIRREGICGKHSEQVPDILQNALFNNMLNTKNCPSLKD 184
 QY 125 KVIILIOACRGQRPGEGVGDDEIVMVIKDS-----PQTIPTYDAL--HV----- 168
 Db 185 KVIILIOACRGD--SPG-----VVMFKDSVGVSGNLSLPTTEFEEDDAIKKHIKDF 234
 QY 169 ---YSTVEGYIAYRHDKGSCFIOTLVDPVFTKRKGHILEL-----LTEVTRMAEALVQ 220
 Db 235 IAFCSSTPDNVSMHPTMGSVFIGRLIE-----HMOEYACSCDVEEIFRKVRPSFEQ 287
 QY 221 EGKARKTNPEIQTSLRKRLYL 241
 Db 288 DGRQMPTE-RVLTTRCFYL 307

RESULT 13
 A56084
 Interleukin-1beta converting enzyme beta isozyme - human
 C:Species: Homo sapiens (man)
 C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
 C:Accession: A56084
 R:Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.
 J. Biol. Chem. 270, 4312-4317, 1995
 A:Title: Cloning and expression of four novel isoforms of human interleukin-1beta conver
 A:Reference number: A56084; MUID:95181414; PMID:7876192
 A:Accession: A56084
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-383 <ALN>
 A:Cross-references: GB:U13697; NID:g717039; PIDN:AAC50107.1; PID:g717040
 C:Genetics:
 A:Gene: IL1BC
 C:Keywords: alternative splicing

Query Match 18.2%; Score 226; DB 2; Length 383;
 Best Local Similarity 29.5%; Pred. No. 3.9e-10;
 Matches 77; Conservative 41; Mismatches 89; Indels 54; Gaps 12;

15 SGALALILCVTK-----AREGSEEDLDALHEMFRLRFESTMKRDPFAEQFOEELKFKQ 69
 Db SRTLALILICNEEFDSPRRTGAEDVDITGTMMLQNLGSDVAKNLTASDMTELEAF 198
 QY 70 QAISREDPVSCAFVLMANG-REGFLKGEDEGV-----KLENLFEALNNKNCALRAKP 124
 Db 199 HRPEHKTS--DSTFLVFMHSGIRREGICGKHSEQVPDILQNALFNNMLNTKNCPSLKD 256
 QY 125 KVIILIOACRGQRPGEGVGDDEIVMVIKDS-----PQTIPTYDAL--HV----- 168
 Db 257 KVIILIOACRGD--SPG-----VVMFKDSVGVSGNLSLPTTEFEEDDAIKKHIKDF 306
 QY 169 ---YSTVEGYIAYRHDKGSCFIOTLVDPVFTKRKGHILEL-----LTEVTRMAEALVQ 220
 Db 307 IAFCSSTPDNVSMHPTMGSVFIGRLIE-----HMOEYACSCDVEEIFRKVRPSFEQ 359

QY 221 EGKARKTNPEIQTSLRKRLYL 241
 Db 360 DGRQMPTE-RVLTTRCFYL 379

RESULT 14
 A42677
 Interleukin-1 beta converting enzyme (EC 3.4.22.-) - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
 C:Accession: A54263; A42677; S21734; S24164
 R:Cerretti, D.P.; Hollingsworth, L.T.; Kozlosky, C.J.; Valentine, M.B.; Shapiro, D.N.; M
 Genomics 20, 468-473, 1994
 A:Title: Molecular characterization of the gene for human interleukin-1beta converting en
 A:Reference number: A54263; MUID:94307734; PMID:8034320
 A:Accession: A54263
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-404 <CE2>
 A:Cross-references: GB:I27475
 R:Gerretli, D.P.; Kozlosky, C.J.; Mosley, B.; Nelson, N.; Van Ness, K.; Greenstreet, T.A
 Science 256, 97-100, 1992
 A:Title: Molecular cloning of the interleukin-1beta converting enzyme.
 A:Reference number: A42677; MUID:92229430; PMID:1373520
 A:Accession: A42677
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-404 <CE2>
 A:Cross-references: GB:M87507; NID:g435598; PIDN:AAA6942.1; PID:g186286
 R:Thornberry, N.A.; Bull, H.G.; Calaycay, J.R.; Chapman, K.T.; Howard, A.D.; Kostura, M.
 J. Ding, G.J.F.; Egger, L.A.; Gaffney, E.P.; Limjoco, G.; Palyha, O.C.; Raju, S.M.; Rol
 cci, M.J.
 Nature 356, 768-774, 1992
 A:Title: A novel heterodimeric cysteine protease is required for interleukin-1beta proces
 A:Reference number: S21734; MUID:9224438; PMID:1574116
 A:Accession: S21734
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-404 <THO>
 A:Cross-references: EMBL:X65019; NID:g33792; PIDN:CAA6153.1; PID:g33793
 R:Kronheim, S.R.; Muma, A.; Greenstreet, T.; Glackin, P.J.; van Ness, K.; March, C.J.; E
 Arch. Biochem. Biophys. 296, 698-703, 1992
 A:Title: Purification of interleukin-1beta converting enzyme, the protease that cleaves t
 A:Reference number: S24164; MUID:92337439; PMID:1321554
 A:Accession: S24164
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 120-135, 'AX', 138-139, 'X', 141-142 <XRO>
 A:Gene: GDB:IL1BC
 A:Cross-references: GDB:132368; OMIM:147678
 A:Map position: 11q23-11q23
 C:Keywords: cysteine proteinase; hydrolase

Query Match 18.2%; Score 226; DB 2; Length 404;
 Best Local Similarity 29.5%; Pred. No. 4.2e-10;
 Matches 77; Conservative 41; Mismatches 89; Indels 54; Gaps 12;

15 SGALALILCVTK-----AREGSEEDLDALHEMFRLRFESTMKRDPFAEQFOEELKFKQ 69
 Db SRTLALILICNEEFDSPRRTGAEDVDITGTMMLQNLGSDVAKNLTASDMTELEAF 219
 QY 70 QAISREDPVSCAFVLMANG-REGFLKGEDEGV-----KLENLFEALNNKNCALRAKP 124
 Db 220 HRPEHKTS--DSTFLVFMHSGIRREGICGKHSEQVPDILQNALFNNMLNTKNCPSLKD 277
 QY 125 KVIILIOACRGQRPGEGVGDDEIVMVIKDS-----PQTIPTYDAL--HV----- 168
 Db 278 KVIILIOACRGD--SPG-----VVMFKDSVGVSGNLSLPTTEFEEDDAIKKHIKDF 327
 QY 169 ---YSTVEGYIAYRHDKGSCFIOTLVDPVFTKRKGHILEL-----LTEVTRMAEALVQ 220

Db 328 IAFCSSTPDNVSWRHPTMGVSFICRLIE-----HMOEYACSDVEEIFRKVRFSFEQP 380
 QY 221 EGRKARTNPEIOSTLRKRLYL 241
 Db 381 DGRQMPTTE-RVLTTRCFYL 400

RESULT 15

B57511
 interleukin-1 beta converting enzyme (EC 3.4.22.-) ICE-rel-III - human
 C/Species: Homo sapiens (man)
 C/Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 01-Dec-2000
 C/Accession: B57511; S62183
 R/Munday, N.A.; Vailancourt, J.P.; Ali, A.; Casano, F.J.; Miller, D.K.; Molineaux, S.M.;
 J. Biol. Chem. 270, 15870-15876, 1995
 A/Title: Molecular cloning and pro-apoptotic activity of ICE-relII and ICE-relIII, membe
 A/Reference number: A57511; MUID:95318183; PMID:7797592
 A/Accession: B57511
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-418 <MUN>
 A/Cross-references: GB:U28015; NID:g975300; PIDN:AA75172.1; PID:g903936
 R/Faucheu, C.; Blanchet, A.M.; Collard-Dutilleul, V.; Lalanne, J.L.; Du-Hercend, A.
 Eur. J. Biochem. 236, 207-213, 1996
 A/Title: Identification of a cysteine protease closely related to interleukin-1-beta-con
 A/Reference number: S62183; MUID:96184899; PMID:8617266
 A/Accession: S62183
 A/Status: preliminary; nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 55-317; L, 319-418 <FAU>
 A/Cross-references: EMBL:X94993; NID:g1155085; PIDN:CAA64450.1; PID:g1155086
 C/Keywords: cysteine proteinase; hydrolase

Query Match 18.2%; Score 225; DB 2; Length 418;
 Best Local Similarity 26.8%; Pred. No. 5.2e-10;
 Matches 68; Conservative 53; Mismatches 85; Indels 48; Gaps 10;

QY 19 LALILCVTK-----AREGSEEDLDALHEMFROLPFESTWKRDPTEAQFOELEKFOQAID 73
 Db 178 LALITCNKTFDLPRANGAHYDIVGKRLQGLGYTVDEKULTARDMESVLRATFARPE 237
 QY 74 SREDPVSCAFVVLMAHG--REGFL---KGEDEMYKLENI,FEALNNKNCQALRAKPKYVI 128
 Db 238 HKSS--DSTFLVLMHGILEGICGTAHKKKKPPDLVDTIFQIFNNRNCLSLKDKPKVII 295
 QY 129 IOACRGEORDPGETVGGDEIVNVIKDSPTIPIYT-----DALHY 169
 Db 236 VOACRGEKH--GE-----LWVRDSPASLAVISSQSSSENLEADSVCKIHEKDFIAC 345
 QY 170 STVEGYIAVRHQKSCFIQTLVDVFTKRK--GHILELTVETRRMAEALVQEGKARKT 227
 Db 346 STPHNVSWRDRGRSIFITELITCFQKYSCCCHMEIF---RKVQKSFVFPQAKQMP 401
 QY 228 NPEIOSTLRKRLYL 241
 Db 402 TIE-RATLTTRDFYL 414

Search completed: February 26, 2003, 12:21:31
 Job time : 27.5139 secs

PI Alnemri ES, Fernandez-Alnemri T;
 XX
 DR MPI: 2000-376558/32.
 XX N-PSDB; AAA15164.
 XX
 PT Novel nucleic acids encoding cell death specific protease termed
 PT caspase-14 useful for treating cancers by stimulating apoptosis -
 XX
 PS Claim 13; Fig 7; 78pp; English.
 XX
 CC The present sequence represents a human caspase-14 polypeptide. The
 CC polypeptide is a cell death specific protease, and is an apoptosis
 CC stimulator. Caspase-14 polynucleotides and polypeptides, and
 CC anti-caspase-14 antibodies are useful for treating or reducing the
 CC severity of pathological conditions associated with increased or
 CC decreased levels of apoptosis. Apoptosis mediated diseases such as
 CC AIDS, neurodegenerative diseases and ischemic injury are treated by
 CC administering anti-caspase-14 antibodies. The antibody is useful for
 CC determining the presence or the level of caspase-14 in tissue sample
 CC and also for the isolation of caspase-14 with apoptotic activity or
 CC in screening assay to identify an agent that inhibits heterodimer or
 CC heterotrimer formation and therefore, apoptosis.
 XX
 SQ Sequence 242 AA;
 Query Match 99.6%; Score 1234; DB 21; Length 242;
 Best local similarity 99.6%; Pred. No. 1.9e-121;
 Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLDALHMFRLRPESTMKRDPTEAQ 60
 DB 1 MSNPRSLSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFRLRPESTMKRDPTEAQ 60
 QY 61 FOEELKFOQALDSREDPVSCAFVVLMAHGREGFLKGEDEGVKLENLFEALNNKNCAL 120
 DB 61 FOEELKFOQALDSREDPVSCAFVVLMAHGREGFLKGEDEGVKLENLFEALNNKNCAL 120
 QY 121 RAKPKVYIIIOACRGQRDPGETVSGDEIWMVTKDSPOTIPYTDALHYSTVEGYIAYRH 180
 DB 121 RAKPKVYIIIOACRGQRDPGETVSGDEIWMVTKDSPOTIPYTDALHYSTVEGYIAYRH 180
 QY 181 DQKSCFIQTLVDVFTKRGHILELLEVTTRMAEALVQEGKARKTNPEIOSTLRKRLY 240
 DB 181 DQKSCFIQTLVDVFTKRGHILELLEVTTRMAEALVQEGKARKTNPEIOSTLRKRLY 240
 QY 241 LQ 242
 DB 241 LQ 242

RESULT 2
 AAG77980
 ID AAG77980 standard; Protein; 242 AA.
 XX
 AC AAG77980;
 XX
 DT 05-APR-2002 (first entry)
 XX
 DE Full-length human caspase-14.
 XX
 KW Human; caspase-14; anti-apoptotic; apoptosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200181595-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 27-APR-2001; 2001WO-US13831.
 XX
 PR 27-APR-2000; 2000US-19962P.
 XX
 PA (KNOL) KNOLL GMBH.

XX
 PI Mankovich JA;
 XX
 DR MPI: 2002-041410/05.
 XX N-PSDB; AAK96248.
 XX
 PT Novel isolated human caspase-14 proteins and nucleic acid sequences,
 PT useful for identifying modulators of caspase-14 protein that are useful
 PT for modulating apoptosis -
 XX
 PS Claim 20; Fig 1; 58pp; English.
 XX
 CC The sequence represents the novel full-length human caspase-14 protein,
 CC referred to as "Caspase-14 NEW" in the specification. The invention
 CC relates to a novel isolated human caspase-14 protein comprising an amino
 CC acid sequence with MSNPRSLSE, at its amino terminus. The caspase-14 of
 CC the invention has anti-apoptotic activity. Caspase-14 acts as a modulator
 CC of caspase-14 activity. The polypeptide is useful for identifying a
 CC compound which is a modulator of human caspase-14 activity, and is also
 CC useful for identifying a target molecule. An antibody to caspase-14 is useful
 CC for isolating the protein by standard techniques, and for detecting
 CC caspase-14 to evaluate the abundance and expression pattern. The antibody
 CC is also useful for diagnostically monitoring protein levels in a tissue
 CC as a part of a clinical testing procedure. The polypeptide is useful as a
 CC protease to cleave substrates and for inducing apoptosis in cells, in
 CC screening assays, and as a bait protein in a two-hybrid or three-hybrid
 CC assay to identify other proteins that interact with human caspase-14
 CC protein.
 XX
 SQ Sequence 242 AA;
 Query Match 99.6%; Score 1234; DB 23; Length 242;
 Best local similarity 99.6%; Pred. No. 1.9e-121;
 Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLDALHMFRLRPESTMKRDPTEAQ 60
 DB 1 MSNPRSLSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFRLRPESTMKRDPTEAQ 60
 QY 61 FOEELKFOQALDSREDPVSCAFVVLMAHGREGFLKGEDEGVKLENLFEALNNKNCAL 120
 DB 61 FOEELKFOQALDSREDPVSCAFVVLMAHGREGFLKGEDEGVKLENLFEALNNKNCAL 120
 QY 121 RAKPKVYIIIOACRGQRDPGETVSGDEIWMVTKDSPOTIPYTDALHYSTVEGYIAYRH 180
 DB 121 RAKPKVYIIIOACRGQRDPGETVSGDEIWMVTKDSPOTIPYTDALHYSTVEGYIAYRH 180
 QY 181 DQKSCFIQTLVDVFTKRGHILELLEVTTRMAEALVQEGKARKTNPEIOSTLRKRLY 240
 DB 181 DQKSCFIQTLVDVFTKRGHILELLEVTTRMAEALVQEGKARKTNPEIOSTLRKRLY 240
 QY 241 LQ 242
 DB 241 LQ 242

RESULT 3
 AAG77984
 ID AAG77984 standard; Protein; 242 AA.
 XX
 AC AAG77984;
 XX
 DT 05-APR-2002 (first entry)
 XX
 DE Full-length human caspase-14 old.
 XX
 KW Human; caspase-14; anti-apoptotic; apoptosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200181595-A2.
 XX

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PD 01-NOV-2001.
XX
XX 27-APR-2001; 2001MO-US13831.
XX
XX 27-APR-2000; 2000US-199962P.
XX
XX (KNOL ) KNOLL GMBH.
XX
XX Mankovich JA;
XX
XX WPI; 2002-041410/05.
XX
XX Novel isolated human caspase-14 proteins and nucleic acid sequences,
XX useful for identifying modulators of caspase-14 protein that are useful
XX for modulating apoptosis -
XX
XX Example; Fig 1; 58pp; English.
XX
XX The sequence represents the full-length human caspase-14 protein,
XX referred to as "Caspase-14 OLD" in the specification. The invention
XX relates to a novel isolated human caspase-14 protein comprising an amino
XX acid sequence with MSNPRSEF, at its amino terminus. The caspase-14 of
XX the invention has anti-apoptotic activity. Caspase-14 acts as a modulator
XX of caspase-14 activity. The polypeptide is useful for identifying a
XX compound which is a modulator of human caspase-14 activity, and is also
XX useful for identifying a compound which modulates the interaction of
XX caspase-14 with a target molecule. An antibody to caspase-14 is useful
XX for isolating the protein by standard techniques, and for detecting
XX caspase-14 to evaluate the abundance and expression pattern. The antibody
XX is also useful for diagnostically monitoring protein levels in a tissue
XX as a part of a clinical testing procedure. The polypeptide is useful as a
XX protease to cleave substrates and for inducing apoptosis in cells, in
XX screening assays, and as a bait protein in a two-hybrid or three-hybrid
XX assay to identify other proteins that interact with human caspase-14
XX protein.
XX
XX Sequence 242 AA;
SQ
Query Match 96.0%; Score 1189; DB 23; Length 242;
Best Local Similarity 99.6%; Pred. No. 1e-116;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 10 EKYDMSGALALILCVTKAREGSEEDLDALHMFROLRFESTMKRDPPTAEQFOEELKFKQ 69
DB 10 EKYMSGARLALILCVTKAREGSEEDLDALHMFROLRFESTMKRDPPTAEQFOEELKFKQ 69
QY 70 QALDSREDPVSCAFVILMAHGREGFLKGEDGEMVLENTLFEALNNKNCQALRAKPKVYII 129
DB 70 QALDSREDPVSCAFVILMAHGREGFLKGEDGEMVLENTLFEALNNKNCQALRAKPKVYII 129
QY 130 QACGSEORDEPETVGGDEIVNWIKDSPOTITPTTDALHVSIVTVEGYIAYRRDQKSCFIQ 189
DB 130 QACGSEORDEPETVGGDEIVNWIKDSPOTITPTTDALHVSIVTVEGYIAYRRDQKSCFIQ 189
QY 190 TLVDVFTKRKHILLETVEVTRMAEALVQEGARKTNPEIOSTLRKRLYLQ 242
DB 190 TLVDVFTKRKHILLETVEVTRMAEALVQEGARKTNPEIOSTLRKRLYLQ 242
RESULT 4
AAV68865
ID AAV68865 standard; Protein; 229 AA.
XX
XX AAV68865;
XX
XX 16-MAY-2000 (first entry)
XX
XX Amino acid sequence of a human caspase-14 polypeptide.
XX
XX Mouse; caspase-14 polypeptide; human; caspase; apoptosis;
XX skin disease; keratinisation; wound healing.
XX
XX Homo sapiens.
OS

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```

XX
XX MO200004169-A1.
XX
XX 27-JAN-2000.
XX
XX 12-JUL-1999; 99MO-EP04939.
XX
XX 17-JUL-1998; 98EP-0202422.
XX
XX (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
XX Van De Craen M, Declercq W, Vandenabeele P, Fiers W;
XX
XX WPI; 2000-182433/16.
XX
XX N-PSDB; AA260684.
XX
XX New murine and human caspase homologues useful for treating skin
XX related disorders -
XX
XX Claim 2; Page 53-54; 68pp; English.
XX
XX The present sequence represents a human caspase-14 polypeptide.
XX The specification also describes a murine caspase-14 polypeptide.
XX Caspases are cysteinyl aspartate-specific proteinases which play a
XX central role in apoptosis. The polypeptides of the invention are related
XX to human and murine caspase-2 and human caspase-9, and possess all of
XX the typical amino acids involved in catalysis, including the QACRG box,
XX and contain no or only a very short prodomain. mRNA expression of the
XX homologues of the invention is predominant in the skin. The caspase-like
XX polypeptides are useful for treating human or animal diseases, such
XX as skin diseases. They are also useful for screening for compounds that
XX modulate its activity, i.e. agonists, antagonists, and inhibitors. The
XX caspase-like polypeptides and polynucleotides are useful for modulating
XX keratinisation, for diagnosing and treating inappropriate wound
XX healing.
XX
XX Sequence 229 AA;
SQ
Query Match 94.1%; Score 1166; DB 21; Length 229;
Best Local Similarity 99.6%; Pred. No. 2.5e-114;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 14 MSGALALILCVTKAREGSEEDLDALHMFROLRFESTMKRDPPTAEQFOEELKFOQAI 73
DB 1 MSGARLALILCVTKAREGSEEDLDALHMFROLRFESTMKRDPPTAEQFOEELKFOQAI 60
QY 74 SREDPVSCAFVILMAHGREGFLKGEDGEMVLENTLFEALNNKNCQALRAKPKVYIIQACR 133
DB 61 SREDPVSCAFVILMAHGREGFLKGEDGEMVLENTLFEALNNKNCQALRAKPKVYIIQACR 120
QY 134 GEORDEPETVGGDEIVNWIKDSPOTITPTTDALHVSIVTVEGYIAYRRDQKSCFIQTLVD 193
DB 121 GEORDEPETVGGDEIVNWIKDSPOTITPTTDALHVSIVTVEGYIAYRRDQKSCFIQTLVD 180
QY 194 VFTKRKHILLETVEVTRMAEALVQEGARKTNPEIOSTLRKRLYLQ 242
DB 181 VFTKRKHILLETVEVTRMAEALVQEGARKTNPEIOSTLRKRLYLQ 229
RESULT 5
AAV93216
ID AAV93216 standard; Protein; 214 AA.
XX
XX AAV93216;
XX
XX 04-SEP-2000 (first entry)
XX
XX Amino acid sequence of a human caspase-14 splice variant.
XX
XX Caspase-14; cell death specific protease; apoptosis stimulator;
XX apoptosis; AIDS; neurodegenerative disease; ischemic injury.
XX
XX Homo sapiens.
OS

```

```

XX Key Location/Qualifiers
FH Active-site 102..106
XX
XX WO200028047-A1.
XX
XX 18-MAY-2000.
XX
XX 29-OCT-1999; 99WO-US25523.
XX
XX 06-NOV-1998; 98US-0187789.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES, Fernandez-Alnemri T;
XX
XX WPI; 2000-376556/32.
XX
XX N-PSDB; AAI15166.
XX
XX Novel nucleic acids encoding cell death specific protease termed
XX caspase-14 useful for treating cancers by stimulating apoptosis -
XX
XX Claim 42; Fig 9; 78pp; English.
XX
XX The present sequence represents a human caspase-14 splice variant. The
XX polypeptide is a cell death specific protease, and is an apoptosis
XX stimulator. Caspase-14 polynucleotides and polypeptides, and
XX anti-caspase-14 antibodies are useful for treating or reducing the
XX severity of pathological conditions associated with increased or
XX decreased levels of apoptosis. Apoptosis mediated diseases such as
XX AIDS, neurodegenerative diseases and ischemic injury are treated by
XX administering anti-caspase-14 antibodies. The antibody is useful for
XX determining the presence or the level of caspase-14 in tissue sample
XX and also for the isolation of caspase-14 with apoptotic activity or
XX in screening assay to identify an agent that inhibits heterodimer or
XX heterotetramer formation and therefore, apoptosis.
XX
XX Sequence 214 AA;
SQ
Query Match 86.0%; Score 1065; DB 21; Length 214;
Best Local Similarity 88.0%; Pred. No. 9.7e-104;
Matches 213; Conservative 0; Mismatches 1; Indels 28; Gaps 1;
QY 1 MSNPRLSEEEKYDMSGALALILCVTKAREGSEBDLALHMFRLQRFESTWKRDPPTAQ 60
Db 1 MSNPRLSEEEKYDMSGARALILCVTKAREGSEB----- 34
QY 61 FOEELKEFQQAIDSRDVPSCAFVVLMAHGREGFLKGEDGEMVLENI.FEALNNKNCQAL 120
Db 35 --EELEKFOQAIDSRDVPSCAFVVLMAHGREGFLKGEDGEMVLENI.FEALNNKNCQAL 92
QY 121 RAKPRVYIIQACRGORDPGEIVGDEITFMVLIKDSPTQITPTVTDALHYVSTVEGYIAYKH 180
Db 93 RAKPRVYIIQACRGORDPGEIVGDEIWMVLIKDSPTQITPTVTDALHYVSTVEGYIAYKH 152
QY 181 DQKSGCFIQLTLDVFTFKRGHILELLETVTRMAEAEALVOEGKARKTNPEIOSTIRKRLY 240
Db 153 DQKSGCFIQLTLDVFTFKRGHILELLETVTRMAEAEALVOEGKARKTNPEIOSTIRKRLY 212
QY 241 LQ 242
Db 213 LQ 214

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```

XX KW Mouse; caspase-like polypeptide; human; caspase; apoptosis;
XX KV skin disease; keratinisation; wound healing.
XX
XX OS Mus musculus.
XX
XX WO200004169-A1.
XX
XX 27-JAN-2000.
XX
XX 12-JUL-1999; 99WO-EP04939.
XX
XX 17-JUL-1998; 98EP-0202422.
XX
XX (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
XX Van De Craen M, Declercq W, Vandenabeele P, Fiers W;
XX
XX WPI; 2000-182433/16.
XX
XX N-PSDB; AAZ60683.
XX
XX New murine and human caspase homologues useful for treating skin
XX related disorders -
XX
XX Claim 1; Page 51-52; 68pp; English.
XX
XX The present sequence represents a murine caspase-like polypeptide. The
XX specification also describes a human caspase-like polypeptide.
XX Caspases are cysteinyl aspartate-specific proteinases which play a
XX central role in apoptosis. The polypeptides of the invention are related
XX to human and murine caspase-2 and human caspase-9, and possess all of
XX the typical amino acids involved in catalysis, including the QACRG box,
XX and contain no or only a very short prodomain. mRNA expression of the
XX homologues of the invention is predominant in the skin. The caspase-like
XX polypeptides are useful for treating human or animal diseases, such
XX as skin diseases. They are also useful for screening for compounds that
XX modulate its activity, i.e. agonists, antagonists, and inhibitors. The
XX caspase-like polypeptides and polynucleotides are useful for modulating
XX keratinisation, for diagnosing and treating inappropriate wound
XX healing.
XX
XX Sequence 257 AA;
SQ
Query Match 75.4%; Score 934.5; DB 21; Length 257;
Best Local Similarity 70.9%; Pred. No. 7e-90;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;
QY 1 MSNPRLSEEEKYDMSGALALILCVTKAREGSEBDLALHMFRLQRFESTWKRDPPTAQ 60
Db 5 MSNPRLSEEEKYDMSGARALILCVTKAREGSEBDLALHMFRLQRFESTWKRDPPTAQ 64
QY 61 FOEELKEFQQAIDSRDVPSCAFVVLMAHGREGFLKGEDGEMVLENI.FEALNNKNCQAL 120
Db 65 FLEELDEFQQTIDNNEEVSCAFVVLMAHGREGFLKGEDGEMVLENI.FEALNNKNCQAL 124
QY 121 RAKPRVYIIQACRGORDPG-----ETVGGDEIWMVLIKDSPTQITPTVTDALHY 168
Db 125 RAKPRVYIIQACRGHRDPGEEELKGNELGDEBELGGE-VAVLKNNQSLPTTDTLHI 183
QY 169 YSTVEGYIAYHHDQSGCFIQLTLDVFTFKRGHILELLETVTRMAEAEALVOEGKARKTN 228
Db 184 YSTVEGYLSYHDEKSGFIQLTLDVFTFKKGSILELLETVTRMAEAEALVOEGKARKTN 243
QY 229 PEIOSTIRKRLYLQ 242
Db 244 PEVOSTIRKRLYLQ 257

```

```

RESULT 6
AA68864
ID AAY68864 standard; Protein; 257 AA.
XX
XX AC AAY68864;
XX
XX 16-MAY-2000 (first entry)
XX
XX Amino acid sequence of a murine caspase-like polypeptide.

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RESULT 7
AAW93592
ID AAW93592 standard; Protein; 281 AA.
XX
XX AC AAW93592;

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XX 21-JUN-1999 (first entry)
 XX Mouse caspase-14 protein.
 DE
 XX Caspase-14; murine; protease; treatment; apoptotic-related disease;
 KM autoimmune disease; cancer; acquired immunodeficiency syndrome; AIDS;
 KM neurodegenerative disease; ischemic injury; anti-idiotypic antibody;
 KM caspase-14 processing activity; epitope; competitor; modulator.
 XX
 OS Mus sp.
 XX
 PN M0910504-A2.
 XX
 PD 04-MAR-1999.
 XX
 PF 26-AUG-1998; 98MO-US17715.
 XX
 PR 26-AUG-1997; 97US-0056986.
 XX
 PA (IDUN-) IDUN PHARM INC.
 XX
 PI Alnemri ES, Fernandez-Alnemri T;
 XX
 DR WPI; 1999-204670/17.
 DR N-PSDB; AAX3515.
 XX
 PT Newly isolated polynucleotide encoding a caspase-14 polypeptide -
 PT useful for identifying (ant)agonists that are useful in the
 PT diagnosis and treatment of apoptosis-related diseases
 XX
 PS Claim 4; Fig 1; 59pp; English.
 XX
 CC This invention describes a novel murine caspase-14 which has protease
 CC activity. The caspase-14 polypeptide is useful for identifying
 CC (ant)agonists of the polypeptide, where enzyme activity is measured
 CC with a fluorescent substrate (especially DEVD-AMC or YVAD-AMC. Activated
 CC caspase-14 is useful for identifying inhibitors or enhancers of
 CC caspase-14 activity. The compounds identified by both methods of
 CC form pharmaceutical compositions for treating apoptotic-related diseases,
 CC including autoimmune disease, cancer, acquired immunodeficiency syndrome
 CC (AIDS), neurodegenerative diseases and ischemic injury. The
 CC anti-caspase-14 antibody is useful for measuring the level of caspase-14
 CC in a tissue sample. An antibody that binds to a caspase-14 polypeptide is
 CC useful for isolating the polypeptide, and an antibody that binds to the
 CC large or small subunit the polypeptide is useful for identifying samples
 CC with caspase-14 processing activity. An antibody that binds to caspase-14
 CC heterodimer or heterotetramer is useful for isolating caspase-14 with
 CC apoptotic activity or in a screening assay to identify (ant)agonists. The
 CC antibodies form kits for such purposes. The anti-caspase-14 antibody is
 CC also useful for preparing anti-idiotypic antibodies, which mimic a
 CC caspase-14 epitope recognized by the anti-caspase-14 antibody. Therefore,
 CC the antibody is useful as a competitor of caspase-14 in reducing the
 CC level of caspase-14 activity, which reduces the level of apoptotic
 CC activity. Oligonucleotides made from the polynucleotides are useful as
 CC polymerase chain reaction (PCR) primers or probes to screen genomic or
 CC cDNA libraries for similar caspase-14 encoding polynucleotides, or for
 CC diagnosis of diseases associated with enhanced or inhibited apoptosis.
 CC The isolated caspase-14 gene permits methods of modulating apoptosis
 CC for the treatment of human diseases.
 CC
 CC
 SO Sequence 281 AA;

Query Match 75.4%; Score 934.5; DB 20; Length 281;
 Best Local Similarity 70.9%; Pred. No. 7.9e-90;
 Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;

1 MSNRSLEEEYDMSGALATILCTYKREGSEEDLALHEMPOLARESTMKDPTAEQ 60
 24 MSDPQLDEEYDMSGALATILCTYKREGSEEDLALHEMPOLARESTMKDPTAEQ 83
 61 FOEELERFOAIDSRDPVSCAFVVLMAHGREGLKGEDEGMVXLNLFALNNKNCAL 120

DB 84 FLEELDFEFOOTIDNWEPEVSCAFVVLMAHGEGLKGEDEKMRLEDLFEVLNNKNCAL 143
 QY 121 RAKPKVYIIQACRGEORDPG-----ETVSGDEIYMWIKSPOTIPYTDALHV 168
 DB 144 RGRKVTYIIQACRGEHNDPBEELRGNELGDEELGDE-VAVLKNNPQSPITTDLIHI 202
 QY 169 YSTVEGYIAYRHDKGSCFIQTLVDVFTKRGHILLLTEVTRMAEALVQEGKARTN 228
 DB 203 YSTVEGYLSYRHDEKSGFQTLVDVFIHKKSILLETETRLMANTVWQEGKPRKN 262
 QY 229 PEIQTSLRKRLYLQ 242
 DB 263 PEVQSTLRKRLYLQ 276

RESULT 8
 ID AAY93213 standard; Protein; 281 AA.
 AC AAY93213;
 XX
 DT 04-SEP-2000 (first entry)
 XX
 DE Amino acid sequence of a murine caspase-14.
 XX
 KM Caspase-14; cell death specific protease; apoptosis stimulator;
 KM apoptosis; AIDS; neurodegenerative disease; ischemic injury.
 XX
 OS Mus sp.
 XX
 FH Key
 FH Region Location/Qualifiers
 FT 1..156
 FT Active-site 134..138
 FT Cleavage-site 156..157
 FT Cleavage-site 162..163
 FT Region 163..257
 FT /note="small subunit"
 XX
 PN M0200028047-A1.
 XX
 PD 18-MAY-2000.
 XX
 PF 29-OCT-1999; 99MO-US25523.
 XX
 PR 06-NOV-1998; 98US-0187789.
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Alnemri ES, Fernandez-Alnemri T;
 XX
 DR WPI; 2000-376558/32.
 DR N-PSDB; AAA15163.
 XX
 PT Novel nucleic acids encoding cell death specific protease termed
 PT caspase-14 useful for treating cancers by stimulating apoptosis -
 XX
 XX Claim 52; Fig 1; 78pp; English.
 XX
 CC The present sequence represents a murine caspase-14 polypeptide. The
 CC polypeptide is a cell death specific protease, and is an apoptosis
 CC stimulator. Caspase-14 polynucleotides and polypeptides, and
 CC anti-caspase-14 antibodies are useful for treating or reducing the
 CC severity of pathological conditions associated with increased or
 CC decreased levels of apoptosis. Apoptosis mediated diseases such as
 CC AIDS, neurodegenerative diseases and ischemic injury are treated by
 CC administering anti-caspase-14 antibodies. The antibody is useful for
 CC determining the presence or the level of caspase-14 in tissue sample
 CC and also for the isolation of caspase-14 with apoptotic activity or
 CC in screening assay to identify an agent that inhibits heterodimer or
 CC heterotetramer formation and therefore, apoptosis.
 CC
 CC
 SO Sequence 281 AA;

XX	PI	Miura M, Yuan J;
XX	XX	WPI, 1995-051742/07.
DR	DR	N-PSDB; AAQ79971.
XX	XX	Promoting or preventing programmed cell death in vertebrate cells
PT	PT	- by inhibiting the activity of interleukin-1 beta converting
XX	XX	enzyme.
PS	PS	Example 5; Fig 12A; 116pp; English.
XX	XX	AAQ79971 encodes AAR66771 human interleukin-1 beta converting enzyme
CC	CC	ced 3 homolog Ich-1(L), increasing Ich-1(L)s enzymatic activity can
CC	CC	promote the programmed cell death of cancer cells (pref. those
CC	CC	overexpressing the bcl-2 oncogene), this can be used as the basis
CC	CC	of a new cancer treatment. Alternatively by reducing Ich-1(L)s
CC	CC	enzymatic activity programmed cell death can be inhibited, this may
CC	CC	be useful in the development of new cell lines which remain viable in
CC	CC	culture for extended or indefinite periods, independent of growth
CC	CC	factors.
XX	XX	
SQ	SQ	Sequence 435 AA;
		Query Match 23.3%; Score 289; DB 16; Length 435;
		Best Local Similarity 31.1%; Pred. No. 1.4e-21;
		Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps
OY	29	REGSEEDLALHEHMFQRLPFESTMKRDPABOPQELKFKQOIDSREDPVSQAFVLMNA 88
DB	202	RGGGDVHSHLVTLFLKLGIDVHVLCDOTAOEQELQNPAQ_LPHARYTDSQ_IYALLS 259
OY	89	HGREGLKGEDEEMVLENIPEALNNKNCQALRAKPKVYIIQACRGEQDPG----- 140
DB	260	HGVEGAIYGVDDKLIQLQGVFLFDNANCPSLQNKPKMEFIQACRGEDETRDGVDDQDGN 319
OY	141	-----ETVGGDEIVMWIKDSPOIPIPYTDALHYSTVEGYIAYRHQKSGSCFIOTLV 192
DB	320	HAGSPGCESSDAKGE-----KLPKMRLLPTRSDMTCGYACUKGTAMRNTRYGSGWYELAA 374
OY	193	DVFTPKR--KGHILELITTEVTRMAEALVQEGKARKTN-----PEIOSTLRKRLYL 241
DB	375	QVFSEACGMHVAADMVKVNNALIKD---REGVAPGEFFHRCKEMEYCGSTLCRHLYL 428
		RESULT 13
		AAR98462
ID	ID	AAR98462 standard; Protein; 435 AA.
XX	XX	
AC	AC	AAR98462;
DT	DT	25-SEP-1996 (first entry)
XX	XX	
DE	DE	Human Ice-ced-3 homologue-1L.
XX	XX	
KW	KW	Ich-1L; human ICE-ced-3 homologue; programmed cell death;
KW	KW	apoptosis; interleukin-1 beta converting enzyme; gene therapy.
XX	XX	
OS	OS	Homo sapiens.
XX	XX	
FH	FH	Key Location/Qualifiers
FT	FT	Domain 301..305
FT	FT	/label= QACRG_active_domain
XX	XX	
PN	PN	W09620721-A1.
PD	PD	11-JUL-1996.
XX	XX	
PF	PF	04-JAN-1996; 96WC-US00177.
XX	XX	
PR	PR	04-JAN-1995; 95US-0368704.
XX	XX	
PA	PA	(GEHO) GEN HOSPITAL CORP.

XX	Miura M, Yuan J;	
PI		
XX	WPI: 1996-333763/33.	
DR	N-PSDB; AAT31552.	
XX		
PT	Preventing or promoting programmed cell death in vertebrate cells	-
PT	comprises inhibiting or increasing the activity of	
PT	interleukin-1-beta converting enzyme, or altering expression of	
PT	other related genes	
XX		
PS	Claim 19; Fig 10A; 127pp; English.	
XX		
CC	A novel human cell death gene, designated Ich-1 (ICE-ced3	
CC	homologue-1), was identified as a new member of the ced-3/ICE family.	
CC	Ich-1 is alternatively spliced into 2 different forms. Ich-1L cDNA	
CC	(AAT31552) encodes a 435-amino acid protein (AAR98462) that is	
CC	homologous to the p20 and p10 subunits of human interleukin-1-beta	
CC	converting enzyme (ICE). Ich-1S cDNA (AAT31553) encodes a 312-amino	
CC	acid protein (AAR98463) that is a truncated version of Ich-1L that	
CC	terminates 21 residues after the QACKG active domain of Ich-1L.	
CC	Overexpression of Ich-1L induces Rat-1 fibroblast cells to die in	
CC	culture, but overexpression of Ich-1S suppresses Rat-1 cell death.	
CC	Ich-1L and Ich-1S are useful in methods of controlling programmed	
CC	cell death of vertebrate cells.	
XX		
SQ	Sequence 435 AA;	
	Query Match 23.3%; Score 289; DB 17; Length 435;	
	Best Local Similarity 31.1%; Pred. No. 1.4e-21;	
	Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps	
		7,
OY	29 REGSEDDALEHMFROQRFESTMKRDP7AEOFOELEKFOQATISREDPPVSCAVIYMA 88	
	: : : : : : : : : : : : : : : : : : : : :	
DB	202 RSGGVVDHSTVLTFLFKLGYDVHVALCDOTAQEMQKLNFAO-LEAHRYTDSG-IVALLS 259	
OY	89 HREGEFLKGEDEWVYKLENTFELANNKCOALRAKPKXYIIQACRGEORPS- 140	
	: : : : : : : : : : : : : : : : : : : : :	
DB	260 HVEGATIGYVDKSLQLOQVFLPDMNANCPSLQNKPKKFFIOACRGEIDRDVDDQDGN 319	
OY	141 -----ETVGGDEIVWYIKDSPQTIPTTYDALTHVSTEGYIAYRHDDQKSCFTIQLTV 192	
	: : : : : : : : : : : : : : : : : : : : :	
DB	320 HAGSPGCESDSAGKE-----KLPKRRLPTRSPMICGYACLKGTAMRMVTKRGSWYIEALA 374	
OY	193 DVFETKR--KGHLELLETTYTRMAAEALVEQEKARKTN-----PEQSTLRKKLYL 241	
	: : : : : : : : : : : : : : : : : : : : :	
DB	375 QVFSEKACMHVADWLKVYNALIKD---REGYAGCTEFHCKEMSEYCTLCRHLYL 428	
	: : : : : : : : : : : : : : : : : : : : :	
	RESULT 14	
ID	AAR90703	
	AAR90703 standard; Protein; 435 AA.	
XX		
AC	AAR90703;	
XX		
DT	10-APR-1996 (first entry)	
XX		
DE	Interleukin-1-beta converting enzyme like apoptosis protease-2.	
XX		
XX	Interleukin-1-beta converting enzyme like apoptosis protease-2;	
KW	ICE-IAP-2; cell death; immunosuppression; AIDS; Alzheimer disease;	
KW	Parkinson disease; septic shock; rheumatoid arthritis; head injury;	
XX	antitumour; antiviral.	
XX		
OS	Homo sapiens.	
XX		
PN	WO9600297-A1.	
XX		
PD	04-JAN-1996.	
XX		
PF	23-JUN-1994; 94WO-US07127.	
XX		
PR	23-JUN-1994; 94WO-US07127.	

XX (HUMA-) HUMAN GENOME SCI INC.
 PA Craig AR, Hastings GA, Hudson PL, Kirkness EF, Wei WH;
 PI MPI; 1996-068881/07.
 DR N-PSDB; AAT15579.
 XX
 XX Interleukin-1 beta converting enzyme like apoptosis protease-1 and
 PT -2 - controls programmed cell death, used in treatment of
 PT immunosuppression related disorders, e.g. AIDS and Alzheimer's
 PT disease
 PS Claim 1; Fig 2A-C; 58pp; English.
 XX
 CC Human interleukin-1-beta converting enzyme like apoptosis protease-2
 CC (ICE-LAP-2) (AA990703) is structurally related interleukin-1-beta
 CC converting enzyme, which is responsible for apoptosis. Recombinant
 CC ICE-LAP-2 is obtd. by expression of encoding cDNA (AAT15579) in
 CC prokaryotic or eucaryotic host cells. It is used to treat diseases
 CC related to abnormally controlled programmed cell death, to control
 CC vertebrate development and tissue homeostasis, to overcome viral
 CC infections and to treat immunosuppression-related disorders.
 CC
 SQ Sequence 435 AA;
 XX
 Query Match 23.3%; Score 289; DB 17; Length 435;
 Best Local Similarity 31.1%; Pred. No. 1,4e-21;
 Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;
 QY 29 REGSEEDLDALEHMFROLRFESTMKRDPATAQFOELEKFOQADISREDPVSCAFVILMA 88
 DB 202 RSGGDVHDSTLVTLFKLIGDVHVLCDOQAEMOEKLNFAQ-LPARHVTDS-IVALLS 259
 QY 89 HGRGFLKGEDEVKLENLEALNNKQCALRAKPVYIIQACRGORDPG----- 140
 DB 260 HGVEGAIYGVNDKQLQLEVFQLEFQFNANCPSONKPKMFIOACRGDETRDGVQDQDGN 319
 QY 141 -----ETVGSDEIVWIKDSPTIPTYDALHVSIVGVIAYRHDOGSCFIOTLV 192
 DB 320 HAGSPGCEESDAGKE-----KLPRKRLPTRSDMTCGYACLGTAAMNTKSGSWIEMLA 374
 QY 193 DVFTKR--KGHILELLEVTTRMAEALVOEGKARKTN-----PEIOTSLRKRLYL 241
 DB 375 QVFSBRGDMHIVADMLVKNALIKD---REGVAPGTEFHRCKEMSEYCSLTCRHLVL 428
 RESULT 15
 AAM26274
 ID AAM26274 standard; Protein; 435 AA.
 XX
 AC AAM26274;
 XX
 DT 14-APR-1998 (first entry)
 XX
 DE Cell death protein ICH-11.
 XX
 KW cell death; ICH-11; interleukin-1 beta; apoptosis; treatment;
 KW IL-1; tumour; oncogenic transformation; IL-1 receptor antagonist;
 KW IL-1ra; IL-1 beta.
 XX
 OS Homo sapiens.
 XX
 PN MO9733606-A1.
 PD 18-SEP-1997.
 XX
 PF 15-MAR-1996; 96WO-US03468.
 XX
 PR 15-MAR-1996; 96WO-US03468.
 PA (GEHO) GEN HOSPITAL CORP.
 XX

PI Friedlander R, Yuan J;
 XX
 DR MPI; 1997-470641/43.
 DR N-PSDB; AAT90565.
 XX
 XX Preventing apoptosis by blocking binding of interleukin-1beta to its
 PT receptor - useful for, e.g. treating tumours, and inhibiting
 PT oncogenic transformation
 PS Example 5; Fig 7; 42pp; English.
 XX
 CC This is a cell death protein ICH-11. The cell death caused by this
 CC ICH-11 can be prevented by a new method using IL-1 receptor antagonist
 CC (IL-1ra). IL-1ra is also used in a method for preventing programmed cell
 CC death by blocking the binding of interleukin-1 beta (IL-1 beta) to its
 CC receptor. Other methods for modulating programmed cell death are provided
 CC in the specification like a method of modulating apoptosis by activating
 CC the IL-1 beta converting enzyme (ICE) pathway and IL-1 beta production,
 CC a method for altering levels of hypoxia-induced cell death by blocking
 CC IL-1-mediated signal transduction, a method for killing oncogenically
 CC transformed cells by stimulating apoptosis with IL-1 beta or tumour
 CC necrosis factor alpha (TNF alpha), a method of inhibiting hypoxia-induced
 CC cell death by transfecting cells with the CrmA gene (of cowpox), and a
 CC method for modulating apoptosis by downregulating the IL-1 receptor.
 CC IL-1ra inhibits apoptosis induced by trophic factor depletion or hypoxia,
 CC while mature IL-1 beta induces cell death through a pathway independent
 CC of CrmA-sensitive gene activity, and cooperates with ICE and ICH-11 in
 CC apoptosis. Pro-IL-1 beta is the first substrate of any apoptosis-inducing
 CC gene. Increasing/decreasing cells death can be used for the treatment of
 CC tumours (or other conditions where apoptosis is involved). Altering cell
 CC death can also be used for inhibiting oncogenic transformation, and to
 CC treat complications involving apoptosis in cases of hypoxia or ischaemia.
 CC The methods can also be used to screen for agents that modulate
 CC apoptosis. When IL-1 beta is produced endogenously (via ICE) it mediates
 CC cell death, but when added exogenously it may stimulate death if it binds
 CC to its receptor after application of apoptotic stimulus or inhibit it by
 CC binding to the receptor before application of the stimulus.
 CC
 SQ Sequence 435 AA;
 XX
 Query Match 23.3%; Score 289; DB 18; Length 435;
 Best Local Similarity 31.1%; Pred. No. 1,4e-21;
 Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;
 QY 29 REGSEEDLDALEHMFROLRFESTMKRDPATAQFOELEKFOQADISREDPVSCAFVILMA 88
 DB 202 RSGGDVHDSTLVTLFKLIGDVHVLCDOQAEMOEKLNFAQ-LPARHVTDS-IVALLS 259
 QY 89 HGRGFLKGEDEVKLENLEALNNKQCALRAKPVYIIQACRGORDPG----- 140
 DB 260 HGVEGAIYGVNDKQLQLEVFQLEFQFNANCPSONKPKMFIOACRGDETRDGVQDQDGN 319
 QY 141 -----ETVGSDEIVWIKDSPTIPTYDALHVSIVGVIAYRHDOGSCFIOTLV 192
 DB 320 HAGSPGCEESDAGKE-----KLPRKRLPTRSDMTCGYACLGTAAMNTKSGSWIEMLA 374
 QY 193 DVFTKR--KGHILELLEVTTRMAEALVOEGKARKTN-----PEIOTSLRKRLYL 241
 DB 375 QVFSBRGDMHIVADMLVKNALIKD---REGVAPGTEFHRCKEMSEYCSLTCRHLVL 428
 Search completed: February 26, 2003, 12:19:03
 Job time : 31.8526 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 26, 2003, 12:17:35 ; Search time 28.4861 Seconds

(without alignments)
877.445 Million cell updates/sec

Title: US-09-989-903-2

Perfect score: 1350

Sequence: 1 KPMESEMSDPOPLQERYD.....KPRKNPEVQSTLRKLYLQ 260

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	940.5	69.7	242	2 JC7517	caspase-14/a - hum
2	281	20.8	277	2 JC5410	CPP32 protein - mo
3	274.5	20.3	435	2 A54821	apoptosis regulato
4	274.5	20.3	452	2 JC6507	caspase-2 - rat
5	273	20.2	277	2 A55315	cysteine proteinas
6	268	19.9	454	2 JC7123	caspase-9 long cha
7	265	19.6	277	2 SC64710	cysteine proteinas
8	255.5	18.9	212	2 I67437	cysteine proteinas
9	253	18.7	416	2 G02635	ICE-LAP6 - human
10	253	18.7	503	2 A49429	interleukin-1 beta
11	231.5	17.1	495	2 T20038	hypothetical prote
12	219	16.2	182	2 I67436	interleukin-1 beta
13	215.5	16.0	311	2 B56084	interleukin-1 beta
14	215.5	16.0	383	2 A56084	interleukin-1 beta
15	215.5	16.0	404	2 A42677	interleukin-1 beta
16	203	15.0	418	2 B57511	interleukin-1 beta
17	201.5	14.9	402	2 A46495	IL-1 beta converta
18	200	14.8	312	2 B54821	apoptosis regulato
19	190.5	14.1	377	2 A57511	interleukin-1 beta
20	188.5	14.0	263	2 C56084	interleukin-1 beta
21	186	13.8	826	2 T43638	caspase-related pr
22	156	11.6	536	2 T43633	hypothetical prote
23	154	11.4	488	2 T13385	hypothetical prote
24	147.5	10.9	642	2 T27021	interleukin-1 beta
25	142	10.5	136	2 I53300	interleukin-1 beta
26	102	7.6	1429	2 S16233	nitric-oxide synth
27	99	7.3	505	2 S39520	H+-transporting tw
28	97.5	7.2	819	2 T19351	hypothetical prote
29	96.5	7.1	248	2 C82376	amino acid ABC tra

30	95.5	7.1	843	2 A47132	major vault protei
31	95.5	7.1	880	2 F75103	conserved hypochet
32	94.5	7.0	1095	2 PC1114	SKC225 protein -
33	94	7.0	617	2 D96978	hypothetical prote
34	94	7.0	1875	2 S38173	myosin-like protei
35	93.5	6.9	747	2 D95862	probable sensor ha
36	93	6.9	544	2 A42464	microbial metallo
37	92.5	6.9	952	2 D86179	hypothetical prote
38	92.5	6.9	1093	2 A40793	phosphorylase kin
39	92.5	6.9	1093	2 A31758	phosphorylase kin
40	92.5	6.9	1156	2 B70356	chromosome assembl
41	92	6.8	700	2 E69146	senory transducti
42	91.5	6.8	469	2 S17813	circ protein - Rho
43	91.5	6.8	1920	2 A53188	perlecanin - mous
44	91.5	6.8	2670	2 A46719	inositol 1,4,5-tri
45	91	6.7	971	2 A70179	exodeoxyribonuclea

ALIGNMENTS

RESULT 1

JC7517 caspase-14/a - human

C:Species: Homo sapiens (man)

C>Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

C/Accession: JC7517

R:Beckhart, L.; Ban, J.; Fischer, H.; Tschachler, E.

Biochem. Biophys. Res. Commun. 277, 655-659, 2000

A>Title: Caspase-14: Analysis of gene structure and mRNA expression during keratinocyte

A/Reference number: JC7517; MUID:20517231; PMID:11062009

A/Contents: Epidermal keratinocytes

A/Accession: JC7517

A/Molecule type: mRNA

A/Residues: 1-242 <ECK>

C/Cross-references: GB:AF097874

C/Comment: This enzyme accumulates during keratinocyte differentiation and is activated

C/Genetics:

A:Gene: casp-14/a

A/Map position: 19p13.1

A/Intons: 9/3; 59/3; 135/1; 174/1; 208/3

C/Keywords: differentiation

Query Match 69.7%; Score 940.5; DB 2; Length 242;
Best local Similarity 71.3%; Pred. No. 2.1e-63;
Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;

QY	8	MSDPQLOERYDMSGARLALTLCTKARGSEVDMALRMPFYLKFESTMKSDPTAAQ	67
DB	1	MSNRSLEEEKYDMSGARLALTLCTKARGSEVDMALRMPFYLKFESTMKSDPTAAQ	60
QY	68	PLELDFEFTIDNMEPVSQAFVLMAGBEGILLKSEDEKMRVLEDFEVLNKKCAL	127
DB	61	FOELERFOQALISREDPVSCAFVLMAGBEGILLKSEDEKMRVLEDFEVLNKKCAL	120
QY	128	RGRKVVIIACRGSEHDPBELRGNEELGGDE-VAVYKKNPSPPTPTDLHI	186
DB	121	RAKRVIIICRGSEHDPG-----ETVGSDDELVMVTKSDPQITPTDLDLV	168
QY	187	YSTVEGLYSRHDEKSGFIOTLDFVIRKKSILLETBEITRLMANTVEQSEKPRKV	246
DB	169	YSTVEGLYAVRHQKSGFIOTLDFVIRKKSILLETBEITRLMANTVEQSEKPRKV	228
QY	247	PEVOSTLRKRLYLQ 260	
DB	229	PEIOSTLRKRLYLQ 242	

RESULT 2

JC5410 CPP32 protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999

C/Accession: J05410
 R/Muhsag, T.; Uraae, K.; Momoi, M.Y.; Kimura, I.; Momoi, T.
 Biochem. Biophys. Res. Commun. 231, 770-774, 1997
 A/Title: Specific expression of CPP32 in sensory neurons of mouse embryos and activation
 A/Reference number: J05410; MUID:97224429; PMID:9070890
 A/Accession: J05410
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-277 <MUR>
 A/Cross-references: DDBJ:D86352
 A/Experimental source: embryo
 C/Comment: This protein is involved in the apoptosis of dorsal root ganglia neurons.

Query Match 20.8%; Score 281; DB 2; Length 277;
 Best Local Similarity 30.8%; Pred. No. 7,5e-14;
 Matches 82; Conservative 45; Mismatches 91; Indels 48; Gaps 10;

Qy 16 EERYMSGARLALTLCTV-----KARGSEVDMEALERMFRYKFESTMKRDPTA 65
 Db 34 DSSYKMDPEMIGICITITKNFKHKGSTGMSRSGTVDANLRETFMGLKYEVNKNKDLTR 93
 Qy 66 QQFLLEDFEQTIDNWEPPVSCAFV-VLMAGEGLKGDEBKAVRLDLEVLNNKC 124
 Db 94 EIMELMD---SVSKEDHSKRSFVCVILSHGDEGVIFGTNGP-VDLKRLTSFRRGDC 148
 Qy 125 KALRQPKVYIIQACRGEHRDPGEELRGNEELGDEBELGDEVAVLKNNPQSIPTYDTL 184
 Db 149 RSLTKPKFLFIQACRGITLDCGIE---TDSGTDEMA-----CQKIPVHADPL 194
 Qy 185 HIYSTEGLSYRHDKSGSFIQTITD--VFHKKGSILEETRIEMANTEVMOEQK 241
 Db 195 YAVSTAPGYSSWRNSKDGSMFIQSLCSMKLYAHK---LEFMHILTRV--NRKVATEPE 248
 Qy 242 -----PRKVNPEVOSTLRKKLY 258
 Db 249 SFSLDSTPHAKQIPCIIVSMLTRELY 274

RESULT 3

A54821
 Apoptosis regulator ICH-1, stimulatory form L - human
 C/Species: Homo sapiens (man)
 C/Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
 C/Accession: A54821
 R/Mang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
 Cell 78, 739-750, 1994
 A/Title: Ich-1, an Ice/ced-3-related gene, encodes both positive and negative regulators
 A/Reference number: A54821; MUID:94373811; PMID:8087842
 A/Accession: A54821
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-435 <MAN>
 A/Cross-references: GB:U13021; NID:9537291; PID:9537292
 C/Keywords: alternative splicing; apoptosis

Query Match 20.3%; Score 274.5; DB 2; Length 435;
 Best Local Similarity 29.7%; Pred. No. 4e-13;
 Matches 68; Conservative 51; Mismatches 103; Indels 7; Gaps 4;

Qy 36 REGSEVDMEALERMFRYKFESTMKRDPTAQOFLBELDEFOQTIDNWEPPVSCAFVILMA 95
 Db 202 RSGGVDSHTLVTLFRLGVDVHVLCDQVADQEMOEKLNFAQ-LPAHRTDSC-IVALIS 259
 Qy 96 HGEELGLKDEKAVRLDLEVLNNKNCALRGKPKYIIQACRGEHRDPGEELRGNEE 155
 Db 260 HGVEGAIYGVDKLQLOEVFLFDNANCPSLQNKPKMFIQACRDETRDGVDDQDQGN 319
 Qy 156 LGGDEBELGDEVAVLKNNPQSIPTYDTLHIYSTEGLSYRHDKSGSFIQTITDVFH 215
 Db 320 HAQSGCESDQKELPKMRPLPTSDMICGACLCGTAMRNTKGSYIEHLAQVSE 379
 Qy 216 KKGS--ILELTEITRLMANTEVMOEGRP---RKVNPEVOSTLRKKLYL 259

Db 380 RACDMHVADMLVKVNALIKREGYAPGTEFHRCKEMSEYCSILCRHLYL 428

RESULT 4

J06507
 caspase-2 - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C/Accession: J06507
 R/Sato, N.; Milligan, C.E.; Uchiyama, Y.; Oppenheim, R.W.
 Gene 202, 127-132, 1997
 A/Title: Cloning and expression of the cDNA encoding rat caspase-2.
 A/Reference number: J06507; MUID:98087427; PMID:9427555
 A/Accession: J06507
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-452 <SAT>
 A/Cross-references: GB:U77933; NID:g2769705; PIDN:AA896379.1; PID:g2769706

Query Match 20.3%; Score 274.5; DB 2; Length 452;
 Best Local Similarity 30.6%; Pred. No. 4,2e-13;
 Matches 71; Conservative 53; Mismatches 95; Indels 13; Gaps 6;

Qy 36 REGSEVDMEALERMFRYKFESTMKRDPTAQOFLBELDEFOQTIDNWEPPVSCAFVILMA 95
 Db 219 RSGGVDSHTLVTLFRLGVDVHVLCDQVADQEMOEKLNFAQ-LPAHRTDSC-IVALIS 276
 Qy 96 HGEELGLKDEKAVRLDLEVLNNKNCALRGKPKYIIQACRGEHRDPG---EELRG 152
 Db 277 HGVEGAIYGVDKLQLOEVFLFDNANCPSLQNKPKMFIQACRDETRDGVDDQDQGN 336
 Qy 153 NEELGDEBELGDEVAVLKNNPQSIPTYDTLHIYSTEGLSYRHDKSGSFIQTITDV 212
 Db 337 HAQSGCESDQKELMK---MKPLPTSDMICGACLCGTAMRNTKGSYIEHLAQV 393
 Qy 213 FHKKS--ILELTEITRLMANTEVMOEGRP---RKVNPEVOSTLRKKLYL 259
 Db 394 FSRACDMHVADMLVKVNALIKREGYAPGTEFHRCKEMSEYCSILCOQLYL 445

RESULT 5

A55315
 Cysteine proteinase (EC 3.4.22.-) CPP32 precursor - human
 N/Alternate names: cysteine proteinase CPP32
 C/Species: Homo sapiens (man)
 C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000
 C/Accession: A55315; S58899; I39005
 R/Fernandes-Alnemri, T.; Litwack, G.; Alnemri, E.S.
 J. Biol. Chem. 269, 30761-30764, 1994
 A/Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elegans
 A/Reference number: A55315; MUID:95074098; PMID:7983002
 A/Accession: A55315
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-277 <FER>
 A/Cross-references: GB:U13737; NID:g561665; PIDN:AA65015.1; PID:g561666
 R/Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant, M.; Yu, V.L.; Miller, D.K.
 Nature 376, 37-43, 1995
 A/Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammalian
 A/Reference number: S58899; MUID:95319529; PMID:7596430
 A/Accession: S58899
 A/Molecule type: protein
 A/Residues: 29-46;176-189, 'E',191-193 <NTC>
 R/Tewari, M.; Quan, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Poirier, Cell 81, 801-809, 1995
 A/Title: Yama/ CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease
 A/Reference number: A56924; MUID:95292347; PMID:7774019
 A/Accession: I39005
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-189, 'E',191-277 <RES>
 A/Cross-references: EMBL:U26943; NID:g857568; PIDN:AAA74929.1; PID:g857569

C;Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

Query Match 20.2%; Score 273; DB 2; Length 277;

Best Local Similarity 31.5%; Pred. No. 3e-13; Matches 86; Conservative 41; Mismatches 104; Indels 42; Gaps 10;

```

Qy 6 SEMSDPPLQEERYDMGALATLCTVCTK-----AREGSEVDMALERNFRYLK 55
Dy 24 SESWDGSLDINSYKMDYPEMGCLITINNKNFKHSTGNTSGTDVDVANLRFFRNLYK 83
Qy 56 ESTMKRPPTAQOFLBELDEFOQTIDNWEPEVSCAFV-VLMAHGEGLKGEDEKVRLED 114
Dy 84 EVRNKNDLTLR-----EETVELMRDVSKEHSHKSSSFVCLLSHGEGEIIFGTNGP-VDLKK 138
Qy 115 LFEVLNKNCKALRGKPKVYIIQACRGEHRDPGSELNGNEELSGDEVAVLKNP 174
Dy 139 ITNFRGDRCSLTGKPKFLIIQACRGTELDGIE---TDSGD---DDMKCHK--- 186
Qy 175 QSIPTVDTLHIYSTVEGYLSYRDEKSGSFIQTLTDVFIHKKSILELTEITRLMANT 234
Dy 187 --IVDADFLVAYSTAPGYSWRNSKDGSWFIQSLC-AMLVADKLEFMIHLTRV--NR 241
Qy 235 EVMQEGK-----PRKNPEVOSTLRKLY 258
Dy 242 KVATEPESFSDATFHAKKQIPCIIVSMLTKEY 274

```

RESULT 6

caaspase-9 long chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001

Accession: J07123

R;Pujita, E.; Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikkawa, U.; Momoi, T.

Biochem. Biophys. Res. Commun. 264, 550-555, 1999

A;Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9.

A;Reference number: J07123; MUID:20001956; PMID:10529400

A;Accession: J07123

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-454 <FNU>

A;Cross-references: DDBJ:AB019600; NID:96440941; PID:96440942

Query Match 19.9%; Score 268; DB 2; Length 454;

Best Local Similarity 30.2%; Pred. No. 1.3e-12; Matches 74; Conservative 45; Mismatches 96; Indels 30; Gaps 8;

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Qy 36 REGSEVDMALERNFRYLKPESTMKRDPPTAQOFLBELDEFOQTIDNWEPEVSCAFV 95
Dy 218 RTGSNIDRDKLEHFRMLRFVWEVNDLTAKKMTALMEMAH---RNHRALDCFVVILS 274
Qy 96 HGEE-----GLKGEDEKVRLEDLEFVLANKNCKALRGKPKYIIQACRGEHRDGE 148
Dy 275 HGCQASHLQFPGAVYGTGCSVSIEKIVINFGSGCPSLGKPKLFIQACGEGCKHGF 334
Qy 149 ELRGNBELG---GDDELGDEVAVLKNPQ-----SIPVTDTLHIYSTVEGYLS 195
Dy 335 EVACTSSGRLTDSDF---PDATPFGCGRRPLDOLDAVSSLPFTSDILVYSTPFGVS 391
Qy 196 YRHDEKSGSFIQTLTDVFIHKKSILELTEITRLMANTVEWQEGKPRKNPEVOSTLRK 255
Dy 392 WRDKSGSWYIETLDGILFQWARS--EDLQSLLRVANA-VSEKQTYQI-PGCNPLRK 447
Qy 256 KLYVQ 260
Dy 448 KLFKK 452

```

RESULT 7

S64710

cysteine proteinase (EC 3.4.22.-) Cpp32 - Chinese hamster

C;Species: Cricetus griseus (Chinese hamster)

C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999

C;Accession: S64710; S72395

R;Wang, X.; Zelenski, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.

EMBO J. 15, 1012-1020, 1996

A;Title: Cleavage of sterol regulatory element binding proteins (SREBPs) by Cpp32 during

A;Reference number: S64710; MUID:96183185; PMID:8605870

A;Accession: S64710

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-277 <MAN>

A;Cross-references: EMBL:U27463

R;Wang, X.

submitted to the EMBL Data Library, May 1995

A;Reference number: S72395

A;Accession: S72395

A;Molecule type: mRNA

A;Residues: 1-79, 'A', '81-146, 'Y', '148-277 <MAN>

A;Cross-references: EMBL:U27463; NID:91244443; PIDN:AB01511.1; PID:91244444

C;Keywords: apoptosis; cysteine proteinase; hydrolase

Query Match 19.6%; Score 265; DB 2; Length 277;

Best Local Similarity 33.1%; Pred. No. 1.2e-12; Matches 78; Conservative 35; Mismatches 85; Indels 38; Gaps 9;

```

Qy 36 REGSEVDMALERNFRYLKPESTMKRDPPTAQOFLBELDEFOQTIDNWEPEVSCAFV-VLM 94
Dy 64 RSGTDVDAKLRFTFNNLKYEVNRKNDLTLR---EETVELMKNASKEDHSHKSSFFVCVIL 119
Qy 95 AHGEGGLKGEDEKVRLEDLEFVLANKNCKALRGKPKVYIIQACRGEHRDPGSELNGNE 154
Dy 120 SHGDEGVIFGTGDP-IDLKULTSYFRGDRCSLTGKPKFLIIQACRGTELDGIE--TDSGT 178
Qy 155 ELGDEELGDEVAVLKNPQSIPTVDTLHIYSTVEGYLSYRDEKSGSFIQTLTDV--- 211
Dy 179 E-----DDMKC-----QKIPVADFLVAYSTAPGYSWRNSKDGSWFIQSLCMLK 224
Qy 212 VFIHKKSILELTEITRLMANTVEWQEGK-----PRKNPEVOSTLRKLY 258
Dy 225 LVAKH---LEFMIHLTRV--NRKVATEPESFSDSTFHAKKQIPCIIVSMLTKEY 274

```

RESULT 8

I67437

cysteine proteinase (EC 3.4.22.-) P32 - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999

Accession: I67437

R;Flaws, J.A.; Kugu, K.; Tbovovich, A.M.; Desanti, A.; Tilly, K.I.; Hirschfeld, A.N.; Tilly

Endocrinology 136, 5042-5053, 1995

A;Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cell

nulosa cells of the ovarian follicle.

A;Reference number: 153100; MUID:96042508; PMID:7588240

A;Accession: I67437

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-212 <RES>

A;Cross-references: EMBL:U34685; NID:91004370; PIDN:AAC52261.1; PID:91004371

C;Keywords: cysteine proteinase; hydrolase

Query Match 18.9%; Score 255.5; DB 2; Length 212;

Best Local Similarity 31.4%; Pred. No. 4.4e-12; Matches 72; Conservative 38; Mismatches 82; Indels 37; Gaps 9;

```

Qy 16 EERYDMGARGALTLCTV-----KAREGSEVDMALERNFRYLKPESTMKRDPPTA 65
Dy 5 DSSYKMDYPEMGCLITINNKNFKHSTGMSANRGTVDVANLRFTFMALKEVRKNDLTLR 64
Qy 66 QOFLBELDEFOQTIDNWEPEVSCAFV-VLMAHGEGLKGEDEKVRLEDLEFVLANKNCK 124
Dy 65 EIMELND-----SVSKDHSKRSSFVCIILSHGDEGVIFGTNGP-VDLKKLTSFRRGYC 119
Qy 125 KALRGKPKVYIIQACRGEHRDPGSELNGNEELGDEBELGDEVAVLKNPQSIPTVDTL 184
Dy 120 RSLTGKPKFLIIQACRGTELDGIE---TDSGD-----DVVACQKK-----VFEADFL 165

```

Oy 185 HIYSTEVEGLSYRHEDEKSGFIQTL---TDVFHKKGSILELTEITRL 230
 Db 166 YAYSSAPGYISWRNSRGSGWFIQSLCAMLKYAHK---LEPMHILITRY 210

RESULT 9

ICE-LAP6 - human
 C/Species: Homo sapiens (man)
 C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
 C/Accession: G02635
 R/Duan, H.; Oryh, K.; Chinaiyan, A.M.; Poixier, G.G.; Froelich, C.J.; He, W.W.; Dixit, submitted to the EMBL Data Library, April 1996
 A/Reference number: H01513
 A/Accession: G02635
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-416 <DNA>
 A/Cross-references: EMBL:U56390; NID:g1336026; PIDN:AAC50640.1; PID:g1336027

Query Match 18.7%; Score 253; DB 2; Length 416;
 Best Local Similarity 29.1%; Pred. No. 1,6e-11;
 Matches 74; Conservative 47; Mismatches 89; Indels 44; Gaps 8;

Oy 34 KAREGEVDMELERMFRLKFEFTMKRDPDPTAQOFLBELDEFOQTIDNMEEPVSCAFVVL 93
 Db 178 RTRTSNIDCELRFRFSSLHFMVEKGDLTAKKVALILELARDHC---ALDCCVVI 234
 Oy 94 MAHGE-----GLLKGEDEKVRLEDLFEVLNNKCKALRGKPKVYIIQACRGEHRDP 146
 Db 225 LSHGQASHLQPGAVVGTGDCPVSVEKLVNFNGTSCSLGKPKLFIQACGEGQKH 294
 Oy 147 GEELGNELGDEDELGDDEVAVLKNPQ-----SITTYDTLHI 186
 Db 295 GEVASTSP--EDESPQ-----SNPEPDATPQEGLRTEPDDAISLPTSPDIFVS 344
 Oy 187 YSTVGYSYRHEDEKSGFIQTLTDVFIHKKSILELTEITRLMANTEWQEGKPRKN 246
 Db 345 YSTFGFYSWRNSRGSGWVETLIDIF--EQWASEDLQSLIRVANA-VSVKGIYKQW- 400
 Oy 247 PEVOSTLRKKYLQ 260
 Db 401 PCCFNFRLKKLFFK 414

RESULT 10

A49429
 Interleukin-1 beta-converting enzyme homolog CED-3 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
 C/Accession: A49429; T37312
 R/Yuan, J.; Shaham, S.; Ledoux, S.; Ellis, H.M.; Horvitz, H.R.
 Cell 75, 641-652, 1993

A/Title: The C. elegans cell death gene ced-3 encodes a protein similar to mammalian int
 A/Reference number: A49429; MUID:94061982; PMID:8242740
 A/Accession: A49429
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-503 <YUN>
 A/Cross-references: GB:L29052; NID:96503232; PIDN:AAA27982.2; PID:96503233
 A/Note: Sequence extracted from NCBI backbone (NCBIN:139825, NCBI:P:139826)
 A/Accession: T37312
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-417, 'R', 'A', '419-503 <YUN>
 A/Cross-references: EMBL:L29052; PIDN:AAA27982.1
 C/Genetics:
 A/Gene: ced-3
 A/Introns: 45/3; 94/2; 179/1; 289/3; 361/1; 403/3; 483/3

Query Match 18.7%; Score 253; DB 2; Length 503;
 Best Local Similarity 28.9%; Pred. No. 2e-11;

Matches 69; Conservative 49; Mismatches 101; Indels 20; Gaps 7;

Oy 36 REGSEVDMELERMFRLKFEFTMKRDPDPTAQOFLBELDEFOQTIDNMEEPVSCAFVVLMA 95
 Db 259 RNGTRADKDNLTNLFRCMGYIVICKNDLGRGMLLTRDFAK---HSHSDSAILVILS 314
 Oy 96 HGEGLLKGEDEKVRLEDLFEVLNNKCKALRGKPKVYIIQACRGEHRDPGEELRGNEE 155
 Db 315 HGEENVIIQVDDIPISTHEIYDLNLAANAPRLANKPKIVFQACRGERRDGFPVLDSVD 374
 Oy 156 -----LGGEEELG--DEVAVALKNPQSI---PYTDTLHIYSTVEGLSYRHEKG 202
 Db 375 GVPAFLRGMWNRDGPLNFNGCVRPVOQVWRKKPQADILLAVATTAQVSWRNSARG 434
 Oy 203 SGFIQTLTDVF-IHKKG-SILELTEITRLMA-NTEWQEGKPKVNPVOSTLRKKLY 258
 Db 435 SWFIQAVCEVSTAKMDVVELLTVNKKVACGFSQSGSNIUKQPEWTSRLKKFY 493

RESULT 11

T20038
 hypothetical protein C48D1.2 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C/Accession: T20038
 R/Burton, J.
 submitted to the EMBL Data Library, October 1996

A/Reference number: Z19214
 A/Accession: T20038
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-495 <WIL>
 A/Cross-references: EMBL:Z81049; PIDN:CAB02848.1; GSPDB:GN00022; CESP:C48D1.2
 A/Experimental source: clone C48D1
 C/Genetics:
 A/Gene: CESP:C48D1.2
 A/Map position: 4
 A/Introns: 44/3; 93/2; 178/1; 288/3; 360/1; 402/3; 466/1

Query Match 17.1%; Score 231.5; DB 2; Length 495;
 Best Local Similarity 28.3%; Pred. No. 8e-10;
 Matches 60; Conservative 47; Mismatches 86; Indels 19; Gaps 6;

Oy 36 REGSEVDMELERMFRLKFEFTMKRDPDPTAQOFLBELDEFOQTIDNMEEPVSCAFVVLMA 95
 Db 258 RNGTRADKDNLTNLFRCMGYIVICKNDLGRGMLLTRDFAK---HSHSDSAILVILS 313
 Oy 96 HGEGLLKGEDEKVRLEDLFEVLNNKCKALRGKPKVYIIQACRGEHRDPGEELRGNEE 155
 Db 314 HGEENVIIQVDDIPISTHEIYDLNLAANAPRLANKPKIVFQACRGERRDGFPVLDSVD 373
 Oy 156 -----LGGEEELG--DEVAVALKNPQSI---PYTDTLHIYSTVEGLSYRHEKG 202
 Db 374 GVPAFLRGMWNRDGPLNFNGCVRPVOQVWRKKPQADILLAVATTAQVSWRNSARG 433
 Oy 203 SGFIQTLTDVF-IHKKG-SILELTEITRLMA 232
 Db 434 SWFIQAVCEVSTAKMDVVELLTVNKKVYA 465

RESULT 12

I67436
 Interleukin-1-beta-converting enzyme and ced-3 homolog-1, long isoform - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
 C/Accession: I67436
 R/Films, J.A.; Kuuu, K.; Tirovich, A.M.; Desanti, A.; Tilly, K.I.; Hirschfield, A.N.; Tilly, A.
 Endocrinology 136 5042-5053, 1995
 A/Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cel
 lulosa cells of the ovarian follicle.
 A/Reference number: I53300; MUID:96042508; PMID:7588240

A/Accession: I67436
 A/Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 1-182 <RES>
 A:Cross-references: EMBL:U34684; NID:g1004368; PIDN:AAC52260.1; PID:g1004369

Query Match 16.0%; Score 219; DB 2; Length 182;
 Best Local Similarity 32.1%; Pred. No. 2e-09;
 Matches 51; Conservative 39; Mismatches 61; Indels 8; Gaps 4;

Qy 36 REGSEVMEALERMFRYLKFEESTKKRDPDTAQOFLBEELDEFQOTIDNMEEPVSCAFVILMA 95
 Db 22 RSGGDVHTLTLVTLFKLGIVNVHLVDYDTAQEMQEKQNFQQLPAHRYVDSCLVALLS 79
 Qy 96 HGEGLIKGEDEKKNVRLDFEVLNKNCAKRGKPKVYIIQACRGHRDPC--EELRG 152
 Db 80 HGVGGGIVGVGDKLQLQEVFRLFDNANCSLQNKPKMFIIQACRGDETRGVGQQQGN 139

Qy 153 NEELGDEELGDEAVLKNKPNOSIPYTDLHLYSTVE 191
 Db 140 HAQPGCESDVTYKEELMK--MRLPTRSDMTCVYACLK 175

RESULT 13

interleukin-1beta converting enzyme gamma isozyyme - human
 C:Species: Homo sapiens (man)
 C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
 C:Accession: B56084
 R:Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.

J. Biol. Chem. 270, 4312-4317, 1995
 A>Title: Cloning and expression of four novel isoforms of human interleukin-1beta conver
 A:Reference number: A56084; MUID:95181414; PMID:7876192

A:Accession: B56084
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-311 <ALN>
 A:Cross-references: GB:U13698; NID:g717041; PIDN:AAC50108.1; PID:g717042
 C:Gene: IL1BC

C:Keywords: alternative splicing

Query Match 16.0%; Score 215.5; DB 2; Length 311;
 Best Local Similarity 30.3%; Pred. No. 7.1e-09;
 Matches 79; Conservative 43; Mismatches 96; Indels 43; Gaps 13;

Qy 22 SGARLALTLCVTK-----AREGSEVMEALERMFRYLKFEESTKKRDPDTAQOFLBEELDEF 75
 Db 67 SRRRLALICNEERDSTPRRTGAEDVTGKMTMLQNLGIVSVKKNLTASDMTELEAFA 126
 Qy 76 ----QOTIDNMEEPVSCAFVILMAHG-EEGLL-KGEDEK--MVRLEDLFEVLNKNCKA 126
 Db 127 HRPEHKTSDS-----TFIVFMHSHGIRREGICGKKSSEQVDPDILQNALIFNMLNTKNCPS 179
 Qy 127 LRGKPKVYIIQACRGHRDPC-----EELRGNEELGDEELGDEAVLKNKPNOSIPT 179
 Db 180 LKQKPKVYIIQACRGD--SPGVVWFKDSVGSNLSPTTEFEEDD--AIKKAHIEK--- 232
 Qy 180 YTDLHLYSTVEGLSVRHEKSGSFIQTLTDVFIHKKSITLL-TEETRLMANTEVMQ 238
 Db 233 --DFIACSSITPDVNSVRHPTMGSVFIGRLIE--HMQEVACSCDVEIEFRKVFSEOP 287
 Qy 239 EGKPRKVNPEVOSTLRKLYL 259
 Db 288 DGRAQMPTE-RVTLTRCFYL 307

RESULT 14

interleukin-1beta converting enzyme beta isozyyme - human
 C:Species: Homo sapiens (man)
 C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
 C:Accession: A56084
 R:Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.

A>Title: Cloning and expression of four novel isoforms of human interleukin-1beta convert
 A:Reference number: A56084; MUID:95181414; PMID:7876192

A:Accession: A56084
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-383 <ALN>
 A:Cross-references: GB:U13697; NID:g717039; PIDN:AAC50107.1; PID:g717040
 C:Gene: IL1BCE

C:Keywords: alternative splicing

Query Match 16.0%; Score 215.5; DB 2; Length 383;
 Best Local Similarity 30.3%; Pred. No. 9.2e-09;
 Matches 79; Conservative 43; Mismatches 96; Indels 43; Gaps 13;

Qy 22 SGARLALTLCVTK-----AREGSEVMEALERMFRYLKFEESTKKRDPDTAQOFLBEELDEF 75
 Db 139 SRRRLALICNEERDSTPRRTGAEDVTGKMTMLQNLGIVSVKKNLTASDMTELEAFA 198

Qy 76 ----QOTIDNMEEPVSCAFVILMAHG-EEGLL-KGEDEK--MVRLEDLFEVLNKNCKA 126
 Db 199 HRPEHKTSDS-----TFIVFMHSHGIRREGICGKKSSEQVDPDILQNALIFNMLNTKNCPS 251

Qy 127 LRGKPKVYIIQACRGHRDPC-----EELRGNEELGDEELGDEAVLKNKPNOSIPT 179
 Db 252 LKQKPKVYIIQACRGD--SPGVVWFKDSVGSNLSPTTEFEEDD--AIKKAHIEK--- 304

Qy 180 YTDLHLYSTVEGLSVRHEKSGSFIQTLTDVFIHKKSITLL-TEETRLMANTEVMQ 238
 Db 305 --DFIACSSITPDVNSVRHPTMGSVFIGRLIE--HMQEVACSCDVEIEFRKVFSEOP 359

Qy 239 EGKPRKVNPEVOSTLRKLYL 259
 Db 360 DGRAQMPTE-RVTLTRCFYL 379

RESULT 15

interleukin-1 beta converting enzyme (EC 3.4.22.-) - human

C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
 C:Accession: A54263; A42677; S21734; S24164
 R:Gerrett, D.P.; Kozlosky, C.J.; Mosley, B.; Nelson, N.; Van Ness, K.; Greenstreet, T.A.

Science 256, 97-100, 1992
 A>Title: Molecular cloning of the interleukin-1beta converting enzyme.
 A:Reference number: A42677; MUID:92229430; PMID:1373520

A:Accession: A42677
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-404 <CE2>

A:Cross-references: GB:M87507; NID:g435598; PIDN:AAA66942.1; PID:g186286
 R:Thorbertry, N.A.; Bull, H.G.; Calley, J.R.; Chapman, K.T.; Howard, A.D.; Koscute, M.
 J.; Ding, G.J.F.; Egger, L.A.; Gaffney, E.P.; Limjoco, G.; Palyha, O.C.; Raju, S.M.; Rolé
 cci, M.J.

Nature 356, 768-774, 1992
 A>Title: A novel heterodimeric cysteine protease is required for interleukin-1beta proces
 A:Reference number: S21734; MUID:92244338; PMID:1574116

A:Accession: S21734
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-404 <THO>

A:Cross-references: EMBL:X65019; NID:g33792; PIDN:CAA46153.1; PID:g33793
 R:Kornheim, S.R.; Muma, A.; Greenstreet, T.; Glackin, P.J.; van Ness, K.; March, C.J.; I

Arch. Biochem. Biophys. 296, 698-703, 1992

A;Title: Purification of interleukin-1beta converting enzyme, the protease that cleaves
 A;Reference number: S24164; MUID:92337439; PMID:1321594
 A;Accession: S24164
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 120-135, 'AX', 138-139, 'X', 141-142 <KRO>
 C;Genetics:
 A;Gene: GDB:IL1BC
 A;Cross-references: GDB:132368; OMIM:147678
 A;Map position: 11q23-11q23
 C;Keywords: cysteine proteinase; hydrolase

Query Match 16.0%; Score 215.5; DB 2; Length 404;
 Best Local Similarity 30.3%; Pred. No. 9.8e-09;
 Matches 79; Conservative 43; Mismatches 96; Indels 43; Gaps 13;

```

QY 22 SGARLALTLCTK-----ARSGSEVDMELERMFRLKFEESTMKRDPPTAQOFLERLDEF- 75
      ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 160 SRTRLALYICNEEFDSIPRRTGAEVDITGMTMLQNLGYSVDKKNLTASDWTTELEAFA 219
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 76 ----QOTIDNNEEPVSCAFVVIAMHG-EEGLT-KGEDEK--MVRLEDLPFVLYNNKCKA 126
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 220 HRPHEKTSDS-----TFIVFMSHGIRREGICGKKHSEQVPDILQNLAIENMLNTKNCPS 272
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 127 LRGKPKVYIIQACRGEHRDPG-----EELRNEELGGDEELGGDEVAVLKNNPQSIPT 179
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 273 LKDKRKVLI IQCRGD--SPGVWPFKDSVGSVGNLSLPTTEFEFDD--AIKKAHIEK--- 325
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 180 YTDTHIYSTVSGYLSYRDEKSGSFIQTLDVFIHKKSIIEL--TEETRLMANTVEMQ 238
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 326 --DFIAFCSSTPDNYSWRPTNGSVFIQRLIE--HMOEYACSDVEELFRKVRPSPEQP 380
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 239 EGKPRKVNPEVOSTLRKKLYL 259
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 381 DGRAGMPTE-RVTLTRCFYL 400
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: February 26, 2003, 12:21:30
 Job time : 30.4861 secs

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: February 26, 2003, 12:14:00 ; Search time 8.80478 Seconds
(without alignments)
1224.772 Million cell updates/sec

Title: US-09-989-903-2

Perfect score: 1350
Sequence: 1 KPMESEMSDPQLQSERVD.....KPKRVNPEVQSLRKXLYIQ 260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	1332	98.7	257	1	ICEE_MOUSE
2	940.5	69.7	242	1	ICEE_HUMAN
3	290.5	21.5	424	1	ICEE_CHICK
4	276.5	20.5	435	1	ICEE_MOUSE
5	276	20.4	277	1	ICEE_MOUSE
6	274.5	20.3	435	1	ICEE_HUMAN
7	274	20.3	277	1	ICEE_RAT
8	273	20.2	277	1	ICEE_HUMAN
9	263	19.5	277	1	ICEE_CRILLO
10	259.5	19.2	496	1	ICED3_CAEVU
11	255.5	18.9	303	1	ICED3_HUMAN
12	254.5	18.9	303	1	ICED7_MOUSE
13	253	18.7	503	1	ICED3_CAEEL
14	250	18.5	416	1	ICED9_HUMAN
15	249.5	18.5	303	1	ICED7_MESAU
16	249.5	18.5	382	1	ICED7_XENLA
17	243	18.0	339	1	ICED7_MOUSE
18	235	17.4	276	1	ICED7_MOUSE
19	232.5	17.2	293	1	ICED6_HUMAN
20	231.5	17.1	282	1	ICED3_XENLA
21	227.5	16.9	323	1	ICED1_DROME
22	226.5	16.8	299	1	ICED1_SPOFR
23	220	16.3	479	1	ICED8_HUMAN
24	219	16.2	312	1	ICED2_RAT
25	217.5	16.1	386	1	ICED4_XENLA
26	215.5	16.0	404	1	ICED3_HUMAN
27	213	15.8	410	1	ICED3_FELCA
28	211	15.6	404	1	ICED3_CANPA
29	205	15.2	402	1	ICED3_RAT
30	203	15.0	418	1	ICED5_HUMAN
31	201.5	14.9	402	1	ICED3_MOUSE
32	200.5	14.9	405	1	ICED3_HORSE
33	198.5	14.7	404	1	ICED3_PIG

34	198	14.7	521	1	ICED3_HUMAN
35	196.5	14.6	419	1	ICED3_MOUSE
36	190.5	14.1	377	1	ICED3_HUMAN
37	188.5	14.0	373	1	ICED3_MOUSE
38	175	13.0	377	1	ICED3_BOVIN
39	112	8.3	484	1	ICED3_MOUSE
40	102	7.6	1429	1	ICED3_RAT
41	101.5	7.5	480	1	ICED3_HUMAN
42	99	7.3	505	1	ICED3_GALSU
43	95.5	7.1	843	1	ICED3_DICDI
44	95.5	7.1	880	1	ICED3_PIRAB
45	94.5	7.0	1095	1	ICED3_SACKL

ALIGNMENTS

RESULT 1
ICED3_MOUSE
ID ICED3_MOUSE STANDARD; PRT; 257 AA.
AC 089094;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-14 precursor (EC 3.4.22.-) (CASP-14) (MICE) .
GN CASP14.
OS Mus musculus (Mouse) .
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. AND CHARACTERIZATION.
RC STRAIN=C57BL/6J;
RX MEDLINE=99040667; PubMed=9823333;
RA Ahmad M., Srinivasula S.M., Hegde R., Muketash R.,
RA Fernandes-Alnemri T., Alnemri E.S.,
RT "Identification and characterization of murine caspase-14, a new
RT member of the caspase family.";
RT Cancer Res. 58:5201-5205(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Embryo;
RX MEDLINE=99222069; PubMed=10203698;
RA Van de Craen M., Van Loo G., Pye S., Van Crielinge W.,
RA Van den brande I., Molemans F., Fiers W., Declercq W.,
RA Vandenabeele P.,
RT "Identification of a new caspase homologue: caspase-14.";
RT Cell Death Differ. 5:838-846(1998).
RN [3]
RP CHARACTERIZATION AND MUTAGENESIS OF CYS-136.
RX MEDLINE=99009076; PubMed=9792675;
RA Hu S., Shipas S.J., Vincenz C., Salvesen G., Dixit V.M.,
RT "Caspase-14 is a novel developmentally regulated protease.";
RT J. Biol. Chem. 273:29648-29653(1998).
CC -1- FUNCTION: SEEMS TO BE INVOLVED IN THE DEATH RECEPTOR AND GRANZYME
CC B APOPTOTIC PATHWAYS. MAY FUNCTION AS A DOWNSTREAM SIGNAL
CC TRANSDUCER OF CELL DEATH. MAY PLAY A ROLE IN ONTOGENESIS AND SKIN
CC PHYSIOLOGY.
CC -1- SUBUNIT: MAY DIMERIZE WITH LARGE PRODOMAIN CASPASES.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- TISSUE SPECIFICITY: EMBRYO, ADULT LIVER AND LESS IN ADULT BRAIN
CC AND KIDNEY.
CC -1- PM: CLEAVAGE BY GRANZYME B. CASPASE-8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC PROTEASE.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
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DR EMBL; AF092997; AAC63364.1; -.
DR HSSP; P29466; 1ICE.
DR MEROPS; C14.018; -.
DR MGD; MGI:1335092; Casp14.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00655; ICE_p10; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR SMART; SM00115; CASP; 1.
DR PROSITE; PS01121; CASPASE_HIS; FALSE_NEG.
DR PROSITE; PS01122; CASPASE_CYS; FALSE_NEG.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR HydroLase; Thiol protease; Apoptosis; Zymogen.
FT PROPEP 1 7
FT CHAIN 8 ?
FT ACT_SITE 93 257
FT ACT_SITE 136 136
FT MUTAGEN 136 136
FT SEQUENCE 257 AA; 29458 MW; A228D86DFA05B84 CRC64;
Query Match 98.7%; Score 1332; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 4.6e-94;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 MESEMSDPOPLEERYDMSGARLALTLCYTKAREGSEVDMELEHMFRLKFESTMKRRP 63
Db 1 MESEMSDPOPLEERYDMSGARLALTLCYTKAREGSEVDMELEHMFRLKFESTMKRRP 60
Qy 64 TAOQFLBELDEFQOTIDNMEEPVSCAFVVLMAHGEGLKSGDEKXVRLLEDLFEVLNNKN 123
Db 61 TAOQFLBELDEFQOTIDNMEEPVSCAFVVLMAHGEGLKSGDEKXVRLLEDLFEVLNNKN 120
Qy 124 CKAALGKPRVYIIQACRGHRDPGEBELRGNEBELGSGDEVAVLKNPQSIPTTDT 183
Db 121 CKAALGKPRVYIIQACRGHRDPGEBELRGNEBELGSGDEVAVLKNPQSIPTTDT 180
Qy 184 LHIYSTVEGYLSYRHDDEKSGFIQTLTDVFIHKGSILTEETIRLMANTVMOEGKPR 243
Db 181 LHIYSTVEGYLSYRHDDEKSGFIQTLTDVFIHKGSILTEETIRLMANTVMOEGKPR 240
Qy 244 KVNPEVOSTLRKKLYIQ 260
Db 241 KVNPEVOSTLRKKLYIQ 257
RESULT 2
ID ICEE HUMAN STANDARD; PRT; 242 AA.
AC P31944; Q95823;
DT 01-JUL-1993 (Rel. 26, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-14 precursor (EC 3.4.22.-) (CASP-14).
GN CASP14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Brain;
RA Poyet J.-L., Srinivaula S.M., Fernandes-Alnemri T., Alnemri E.S.;
RT "Identification and characterization of human caspase 14."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
[2]

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RP SEQUENCE OF 68-74; 137-147 AND 154-162.
RC Tissue=Keratinocytes;
RX MEDLINE=93162043; PubMed=1286667;
RA Raemussen H.H., van Damme J., Puyse M., Geeser B., Celis J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes."
RL Electrophoresis 13:960-969(1992).
CC -1- FUNCTION: MAY BE INVOLVED IN THE DEATH RECEPTOR AND GRANZYME B
CC APOPTOTIC PATHWAYS. MAY FUNCTION AS A DOWNSTREAM SIGNAL TRANSDUCER
CC OF CELL DEATH.
CC -1- SUBUNIT: MAY DIMERIZE WITH LARGE PRODOMAIN CASPASES.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL; AF097874; AAD16173.1; -.
DR HSSP; P29466; 1ICE.
DR Aarhus/Ghent-2DPAGE; 6109; IEF.
DR MEROPS; C14.018; -.
DR Genew; HGNC:1502; CASP14.
DR MIM; 605848; -.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00655; ICE_p10; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PRINTS; PR00376; IELBCENZME.
DR SMART; SM00115; CASP; 1.
DR PROSITE; PS01121; CASPASE_HIS; FALSE_NEG.
DR PROSITE; PS01122; CASPASE_CYS; FALSE_NEG.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR HydroLase; Thiol protease; Apoptosis; Zymogen.
FT PROPEP 1 ?
FT CHAIN 147 146
FT ACT_SITE 89 89
FT ACT_SITE 132 132
FT SEQUENCE 242 AA; 27679 MW; E539FB78BD808A2 CRC64;
Query Match 69.7%; Score 940.5; DB 1; Length 242;
Best Local Similarity 71.3%; Pred. No. 1.9e-64;
Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;
Qy 8 MSDPOPLEERYDMSGARLALTLCYTKAREGSEVDMELEHMFRLKFESTMKRRP 67
Db 1 MSNPRSLTEERYDMSGARLALTLCYTKAREGSEVDMELEHMFRLKFESTMKRRP 60
Qy 68 FLEELDEFQOTIDNMEEPVSCAFVVLMAHGEGLKSGDEKXVRLLEDLFEVLNNKNKAL 127
Db 61 FOELLEKFOALDSEEDVSCAFVVLMAHGEGLKSGDEKXVRLLEDLFEVLNNKNKAL 120
Qy 128 RGPAPVYIIQACRGHRDPGEBELRGNEBELGSGDEVAVLKNPQSIPTTDTLHI 186
Db 121 RAKPRVYIIQACRGHRDPG-----ETVGGSEIMVVIKDSQTIPTTDAHIV 168
Qy 187 YSTVEGYLSYRHDDEKSGFIQTLTDVFIHKGSILTEETIRLMANTVMOEGKPRVN 246
Db 169 YSTVEGYIAYRHQDQSGCFIQTLTDVFTKRGHILELLEVTBRMAEALVQEGKARKTN 228
Qy 247 PVOSTLRKKLYIQ 260
Db 229 PEIOSTLRKKLYIQ 242

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RESULT 3
ICE2 CHICK STANDARD: PRT; 424 AA.
AC 098943;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-2 precursor (BC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-1L/1S).
GN CASP2 OR ICH1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauvia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White Leghorn; TISSUE=Ovarian granulosa;
RX MEDLINE=97368127; PubMed=9224894;
RA Johnson A.L., Bridgman J.T., Bergeron L., Yuan J.;
RT "Characterization of the avian Ich-1 cDNA and expression of Ich-1L mRNA in the hen ovary";
RL Gene 192:227-233(1997).
CC -|- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. MIGHT FUNCTION BY EITHER
CC ACTIVATING SOME PROTEINS REQUIRED FOR CELL DEATH OR INACTIVATING
CC PROTEINS NECESSARY FOR CELL SURVIVAL (BY SIMILARITY).
CC -|- ALTERNATIVE PRODUCTS: 2 ISOMERS: ICH-1L (SHOWN HERE) AND ICH-1S;
CC ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER IN THE N-AND C-
CC TERMINI. ONLY THE ICH-1L FORM IS FOUND IN THE OVARY.
CC -|- PTM: HETERODIMER OF A SMALL AND A LARGE SUBUNIT (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -|- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -----
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CC or send an email to license@isb-eb.ch).
CC -----
DR EMBL; U64963; AAC29881.1; ALT_INIT.
DR HSSP; P42574; ICP3.
DR MEROPS; C14.006.-;
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00655; CARD; 1.
DR Pfam; PF00655; ICE_p10; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PRINTS; PR00376; IL1BCENZME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PSS0209; CARD; 1.
DR PROSITE; PSS0122; CASPASE_CYS; 1.
DR PROSITE; PSS0121; CASPASE_HIS; 1.
DR PROSITE; PSS0207; CASPASE_P10; 1.
DR PROSITE; PSS0208; CASPASE_P20; 1.
KM Hydrolyase; Thiol protease; Apoptosis; Zymogen; Alternative splicing.
FT PROPEP 1 140
FT CHAIN 141 308 CASPASE-2 SUBUNIT P18 (BY SIMILARITY).
FT CHAIN 309 424 CASPASE-2 SUBUNIT P13 (BY SIMILARITY).
FT DOMAIN 315 424 CASPASE-2 SUBUNIT P12 (BY SIMILARITY).
FT ACT_SITE 248 248 CARD.
FT ACT_SITE 291 291 BY SIMILARITY.
FT VARSPIC 1 7
FT VARSPIC 294 424 MISSING (IN ISOMER ICH-1S).
FT DETRGVDQRGKRSKSGEESDANKENKLRPTRS
FT MTCGACIKGTAAKRNKSGEESDANKENKLRPTRS
FT DMLKVNROIKRGVAPGTEFRCKEMSEYCTLCRDLYL
FT FPGVPGK -> GVSIGIHLPCCCHCICCSMRGTGEMI

FT REMARK:GOIPQAVRVMQTRKISSCVCLHAPI (IN
FT ISOFORM ICH-1S).
SQ SEQUENCE 424 AA; 47959 MW; 792810508B8B2F60 CRC64;
Query Match 21.5%; Score 290.5; DB 1; Length 424;
Best Local Similarity 31.0%; Pred. No. 6.7e-15;
Matches 72; Conservative 53; Mismatches 94; Indels 13; Gaps 5;
QY 36 REGSEVDMEALERMFRLKFEESTKWRDPTAOQFLSELDDEFQOTIDNMEEPSCAFVYLMA 95
DB 190 RSGGDVDCASLELLFKILGQVTFHQDSABEMSEALERSKLPDH--QDVDSIVALLS 247
QY 96 HGEELKGEDEKXVRLLEDLFEVLNNKCALRGKPRVY11OACRGHRDPGEELRGNEE 155
DB 248 HGVEGVGYGTGKLLQGEAFRLFDNANCPNLQNKPKMFFIOACRGDETRGVDRDQKE 307
QY 156 LG--GDEELGDEVAVLKNPQSIPTTYDTLHYSVEGLSTRHBKSGFQTLTDV 212
DB 308 RSDSPGCEESDANKENLK--LRLPTRSDMICGACLKGTAAKRNKSGSWYLEALTIV 364
QY 213 FTH--KKGSITELTEITRLMANTENVQEGKP--RYNPPEVOSTLRKKLYL 259
DB 365 FAEDSRDTHVADMLVKVNRQIKRGVAPGTEFRCKEMSEYCTLCRDLYL 416
RESULT 4
ICE2 MOUSE STANDARD: PRT; 435 AA.
AC P29594; O08737;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-2 precursor (BC 3.4.22.-) (CASP-2) (ICH-1 protease) (NEDD2 protein).
GN CASP2 OR ICH1 OR NEDD2 OR NEDD-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=95047319; PubMed=7958843;
RA Kumar S., Kinoshita M., Noda M., Copeland N.G., Jenkins N.A.;
RT "Induction of apoptosis by the mouse Nedd2 gene, which encodes a
RT protein similar to the product of the Caenorhabditis elegans cell
RT death gene ced-3 and the mammalian IL-1 beta-converting enzyme.";
RL Genes Dev. 8:1613-1626(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenabeele P., Declercq W., van den Brande I.,
RA van de Craen M., Vandenabeele P., Schotte P., van Cleefinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members";
RL FBS Lett. 403:61-69(1997).
RN [3]
RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92328780; PubMed=1378265;
RA Kumar S., Tomooka Y., Noda M.;
RT "Identification of a set of genes with developmentally down-regulated
RT expression in the mouse brain";
RL Biochem. Biophys. Res. Commun. 185:1155-1161(1992).
CC -|- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. MIGHT FUNCTION BY EITHER
CC ACTIVATING SOME PROTEINS REQUIRED FOR CELL DEATH OR INACTIVATING
CC PROTEINS NECESSARY FOR CELL SURVIVAL. MAY BE IMPORTANT IN
CC MULTISTEP CARCINOGENESIS.
CC -|- SUBUNIT: HETERODIMER OF A SMALL AND A LARGE SUBUNIT (BY
CC SIMILARITY).
CC -|- TISSUE SPECIFICITY: HIGH LEVEL EXPRESSION SEEN IN THE EMBRYONIC

CNS, LIVER, LUNG, KIDNEY, SMALL INTESTINE, AND HAIR FOLLICLES OF VIBRISAE. MODERATE EXPRESSION SEEN IN THE SKIN, ORAL MUCOSA, SKLETERAL MUSCLE, SUBMANDIBULAR GLAND AND THYMUS. IN THE ADULT, IT IS HIGHLY EXPRESSED IN SPLEEN, LUNG AND KIDNEY. MODERATELY IN THE BRAIN, HEART, TESTIS, LIVER. LOW LEVELS IN THE THYMUS, SKELETAL MUSCLE, OVARY AND GUT.

-1- DEVELOPMENTAL STAGE: DURING EMBRYONIC DEVELOPMENT IS HIGHLY EXPRESSED IN SEVERAL TYPES OF MOUSE TISSUE UNDERGOING HIGH RATES OF PROGRAMMED CELL DEATH SUCH AS CENTRAL NERVOUS SYSTEM AND KIDNEY.

-1- PIM: THE MATRE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT THAT OF OTHER CASPASES (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.

-1- SIMILARITY: CONTAINS 1 CARD DOMAIN.

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CC -----

DR EMBL: D28492; BAA25876.1; ALT_INIT.

DR EMBL: Y13085; CAA73527.1; ALT_INIT.

DR HSSP: P42574; ICP3.

DR MEROPS: C14.006; -.

DR MGD: MGI:97295; Casp2.

DR InterPro: IPR001315; CARD.

DR InterPro: IPR002398; ICE.

DR InterPro: IPR002138; ICE_p10.

DR InterPro: IPR001309; ICE_p20.

DR Pfam: PF00619; CARD; 1.

DR Pfam: PF00655; ICE_p10; 1.

DR Pfam: PF00656; ICE_p20; 1.

DR PRINTS: PR00376; IL1BCENZYME.

DR SMART: SM00114; CARD; 1.

DR SMART: SM00115; CASc; 1.

DR PROSITE: PS50209; CARD; 1.

DR PROSITE: PS01122; CASPASE_CYS; 1.

DR PROSITE: PS01121; CASPASE_HIS; 1.

DR PROSITE: PS50207; CASPASE_P10; 1.

DR PROSITE: PS50208; CASPASE_P20; 1.

KW Hydrolase; Thiol protease; Apoptosis; Zymogen.

FT PROPEP 1 152

FT CHAIN 153 316

FT CHAIN 317 435

FT CHAIN 331 435

FT DOMAIN 15 103

FT ACT_SITE 260 260

FT ACT_SITE 303 303

FT MUTAGEN 303 303

FT CONFLICT 71 71

SO SEQUENCE 435 AA; 48896 MW; 8984E6AA/6E7A676 CRC64;

Query Match 20.5%; Score 276.5; DB 1; Length 435;

Best Local Similarity 30.6%; Pred. No. 8e-14;

Matches 71; Conservative 53; Mismatches 95; Indels 13; Gaps 6;

QY 36 REGSEVDMEALERMFRYKFESESTMKRDPAAQGFLELDFEQTIDNWEPPSCAFVILMA 95

DB 202 REGGVVDHTTLVTLFLLGLYNVAVLHDQAEWQELQNFQA_LPAHRYVTDSCV_VALLS 259

QY 96 HOEEGLKGEDEKRWLELFEVLNKKKALRGKPKYIIQACREHNDPG---BELRG 152

DB 260 HVEEGIVVDKLTQLQLOEVFRFLFDNANCPSLONKPKMFFIACRDEDTDRGVDDQDGN 319

QY 153 NEELGDEDELGGDEVAVLKNPNQSIPTVDTLHIVSTVGYSYRHDGSGPIOTLTGV 212

DB 320 HVGSGGCEESDAGKEIKM---MRLPTRSDMTCGVACLGNAAMRTKSGSYTEILTV 376

QY 213 FTHKGS--ILBLTEIRILMANTEVMQEGK---RKVNPEVOSTLRKKLYL 259

DB 377 FSEKCDMHDVMDLVKNALIKERGVAPGTEFFHCKEMSEYCTLLCOQLYL 428

RESULT 5

ICE3 MOUSE STANDARD; PRT; 277 AA.

AC P70677; O08668;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama protein) (CPP-32) (Caspase-3) (SREB cleavage activity 1)

DE (SCA-1) (LICE).

GN CASP3 OR CPP32.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;

NP SEQUENCE FROM N.A.

RP MEDLINE=96358624; PubMed=8761296;

RA Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G., Fletcher F.A.;

RT "Molecular characterization of mouse and rat CPP32 beta gene encoding a cysteine protease resembling interleukin-1 beta converting enzyme and CED-3.";

RL Oncogene 13:749-755(1996).

[2]

NP SEQUENCE FROM N.A.

RX MEDLINE=9724429; PubMed=9070890;

RA Mukasa T., Urase K., Momoi M.Y., Kimura I., Momoi T.;

RT "Specific expression of CPP32 in sensory neurons of mouse embryos and activation of CPP32 in the apoptosis induced by a withdrawal of NGF.";

RL Biochem. Biophys. Res. Commun. 231:770-774(1997).

[3]

NP SEQUENCE FROM N.A.

RC STRAIN=C3H/An;

RX MEDLINE=97190206; PubMed=9038361;

RA van de Craen M., Vandenaebale P., Declercq W., van den Brande I., van Loo G., Molemans F., Schotte P., van Crielinge W., Beyaert R., Fiers W.;

RT "Characterization of seven murine caspase family members.";

RL FEBS Lett. 403:61-69(1997).

[4]

NP SEQUENCE FROM N.A.

RP TISSUE=Brain;

RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;

RL Submitted (May-1997) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN. CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY). CLEAVES IL-1 BETA BETWEEN AN ASP AND AN ALA, RELEASING THE MATURE CYOKINE WHICH IS INVOLVED IN A VARIETY OF INFLAMMATORY PROCESSES.

CC -1- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN SPLEEN, LUNG, LIVER, KIDNEY AND HEART. LOWER EXPRESSION IN BRAIN, SKELETAL MUSCLE AND TESTIS.

CC -1- PIV: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND VICE VERSA (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.

CC -----

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CC EMBL; U54803; AAC52768.1; -
 CC EMBL; U54802; AAC52768.1; JOINED.
 CC EMBL; U49929; AAC52764.1; -
 CC EMBL; D86352; BAA21727.1; -
 CC EMBL; Y13086; CAA73528.1; -
 CC EMBL; U19522; AAC5196.1; -
 CC HSSP; P42574; 1PAU.
 CC MEROPS; C14.003; -
 CC MGD; MGI:107739; Casp3.
 CC InterPro; IPR002398; ICE.
 CC InterPro; IPR002138; ICE_p10.
 CC InterPro; IPR001309; ICE_p20.
 CC Pfam; PF00655; ICE_p10; 1.
 CC Pfam; PF00656; ICE_p20; 1.
 CC PRINTS; PR00376; ILBENZYM.
 CC SMART; SM00115; CASc; 1.
 CC PROSITE; PS01122; CASPASE_CYS; 1.
 CC PROSITE; PS01121; CASPASE_HIS; 1.
 CC PROSITE; PS50207; CASPASE_P10; 1.
 CC PROSITE; PS50208; CASPASE_P20; 1.
 CC KX Hydrolyase; Thiol protease; Zymogen; Apoptosis.
 CC FT PROPEP 1 9
 CC FT PROPEP 1 28
 CC FT CHAIN 29 175
 CC FT CHAIN 176 277
 CC FT ACT SITE 121 121
 CC FT ACT SITE 163 163
 CC FT CONFLICT 17 17
 CC FT CONFLICT 51 51
 CC FT CONFLICT 84 84
 CC FT CONFLICT 95 95
 CC FT CONFLICT 97 97
 CC FT CONFLICT 128 128
 CC FT CONFLICT 135 135
 CC SEQUENCE 277 AA; 31474 MW; CE91598f74826605 CRC64;
 Query Match 20.4%; Score 276; DB 1; Length 277;
 Best local Similarity 33.3%; Pred. No. 5e-14;
 Matches 79; Conservativity 39; Mismatches 81; Indels 38; Gaps 9;
 QY 35 ARGGEVDMEALBEMFYKFEETMKRDPPTAQOFLBELDEFOQIDNWEPEVSCAFV-VL 93
 DB 63 SRSGTDVDAANLRETFMGLKYQVNNKNDLTREDILELMD---SVSKEDHSKRSSFCVI 118
 QY 94 MANGEGLGLGDEDEKMYRLDPLFVANNKCKAKRKPKYIIIOACGHRDPGEELRGN 153
 DB 119 LSHGDEGVITGNP-VELKLTLSFFRGDYCRSLTGKPKFIIOACGTGLDCIE---- 173
 QY 154 EELGGEDELGDEVAVALKNNPQSIPTDTLHISTVEGYLSYRHDKSGSGFTITLD-- 211
 DB 174 TDGCTDEEMA-----CQKIPVADFLYAVSTAPGYISWNSKDSGFIOSSLMSL 223
 QY 212 -VPIHKKSLLELTETIRLMANTENVQEGK-----PRKVNPEVQSTLRKKLY 258
 DB 224 KLYAHK---LEFWMILTRV--NRKVATEFESFELDSTFAKKQIPCIIVSLTVELY 274
 RESULT 6
 ICE2_HUMAN STANDARD; PRT; 435 AA.
 AC P42575; P42576;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-1L/1S).

GN CASP2 OR ICH1.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=94373811; PubMed=8087842;
 RA Wang L., Miura M., Bergeron L., Zhu H., Yuan J.;
 RT "Ich-1, an Ice/ced-3-related gene, encodes both positive and negative
 RT regulators of programmed cell death.";
 RL Cell 78:739-750(1994).
 RN [2]
 RP CLEAVAGE SITES.
 RX MEDLINE=96206041; PubMed=8654923;
 RA Xue D., Shaham S., Hotvitz H.R.;
 RT "The Caenorhabditis elegans cell-death protein CED-3 is a cysteine
 RT protease with substrate specificities similar to those of the human
 RT CPP32 protease.";
 RL Gene Dev. 10:1073-1083(1996).
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. MIGHT FUNCTION BY EITHER
 CC ACTIVATING SOME PROTEINS REQUIRED FOR CELL DEATH OR INACTIVATING
 CC PROTEINS NECESSARY FOR CELL SURVIVAL.
 CC -1- SUBUNIT: HETERODIMER OF A SMALL AND A LARGE SUBUNIT (BY
 CC SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, ICH-1L (SHOWN HERE) AND ICH-1S;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER IN THE N-AND C-
 CC TERMINI. ICH-1L ACTS AS A POSITIVE REGULATOR OF APOPTOSIS.
 CC ICH-1S FUNCTIONS AS A NEGATIVE REGULATOR OF APOPTOSIS.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LARGER AMOUNTS IN THE EMBRYONIC
 CC LUNG, LIVER AND KIDNEY THAN IN THE HEART AND BRAIN. IN THE ADULTS
 CC HIGHER LEVEL EXPRESSION IS SEEN IN THE PLACENTA, LUNG, KIDNEY,
 CC PANCREAS THAN IN THE HEART, BRAIN, LIVER AND SKELETAL MUSCLE.
 CC -1- PTM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
 CC THAT OF OTHER CASPASES.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
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 CC or send an email to license@isb-sib.ch).

CC EMBL; U13021; AAA58959.1; -
 CC EMBL; U13022; AAA58960.1; -
 CC HSSP; P29466; 1ICE.
 CC MEROPS; C14.006; -
 CC Genew; HGNC:1503; CASP2.
 CC MIM; 600639; -
 CC InterPro; IPR001315; CARD.
 CC InterPro; IPR002398; ICE.
 CC InterPro; IPR002138; ICE_p10.
 CC InterPro; IPR001309; ICE_p20.
 CC Pfam; PF00619; CARD; 1.
 CC Pfam; PF00655; ICE_p10; 1.
 CC Pfam; PF00656; ICE_p20; 1.
 CC PRINTS; PR00376; ILBENZYM.
 CC SMART; SM00114; CARD; 1.
 CC SMART; SM00115; CASc; 1.
 CC PROSITE; PS50209; CARD; 1.
 CC PROSITE; PS01122; CASPASE_CYS; 1.
 CC PROSITE; PS01121; CASPASE_HIS; 1.
 CC PROSITE; PS50207; CASPASE_P10; 1.
 CC PROSITE; PS50208; CASPASE_P20; 1.
 CC Hydrolyase; Thiol protease; Zymogen; Apoptosis; Alternative splicing.
 CC FT PROPEP 1 152
 CC FT CHAIN 153 308
 CC FT PROPEP 309 316
 CC CASPASE-2 SUBUNIT P18.

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FT CHAIN 317 435 CASPASE-2 SUBUNIT P13.
FT CHAIN 331 435 CASPASE-2 SUBUNIT P12.
FT DOMAIN 15 103 CARD.
FT ACT SITE 260 260 BY SIMILARITY.
FT ACT SITE 303 303 BY SIMILARITY.
FT ACT SITE 303 303 BY SIMILARITY.
FT VARSPLIC 1 14 MISSING (IN ISOFORM ICH-1S).
FT VARSPLIC 306 435 DETDRGVQDQDGNKHAQSPCESDAKKELPKRRLPTNSD
MIQYACTGTAAMRNTRGSGWYIEALQVSEACDMHYA
DMLVKVALLIKDRGVAAGTEFHRCKMSEYCSLCHLYL
PGRHPT -> GGAIGSLGHLLEFTATASLAL (IN
ISOFORM ICH-1S).
FT MUTAGEN 303 303 C-5S: LOSS OF FUNCTION.
FT MUTAGEN 352 352 A-5T: LOSS OF FUNCTION.
SQ SEQUENCE 435 AA; 48855 MW; 1652EC73F6286FB7 CRC64;
Query Match 20.3%; Score 274.5; DB 1; Length 435;
Best Local Similarity 29.7%; Pred. No. 1,le-13;
Matches 68; Conservative 51; Mismatches 103; Indels 7; Gaps 4;
QY 36 RESEVMEALERMPRYLKFEETMKRDPDPAQOFLLEDEFOOTIDNWEPEVSCAFVILMA 95
D 202 RSGGDVDSHTLVTLFKLGYVHVLCDTQAGMOEKLQNFAD-LPAHAYTSC-IVALIS 259
QY 96 HGEGLLKGEDEKRWLEDFEVILNNKCKALRGKPKYV11QACGEHRDPGEELRGNEE 155
D 260 HGVEGAIYGVGKLLQLOEVQLPDMNANCPSLQNKPKKFFIQACGDETDGVDQDQGN 319
QY 156 LGGBELGGEVAVLAKNNPQSTPTTDLHLYSTVEGLYSTRHDKSGGFIQTLTDFPIH 215
D 320 HAGSPGCEESDAGKEKPKMLPTPSDMIQGYACLKTAAMNTRGSGWYIEALQVSE 379
QY 216 KKGS-IILETEITRLMANTENVMOEGKP--RKVNPEVOSTLRKLYL 259
D 380 RACDMHVAADMVKKVALLIKDRGVAAGTEFHRCKMSEYCSLCHLYL 428
DB
RESULT 7
ICE3 RAT STANDARD: PRT: 277 AA.
AC P55213; P70543; Q62993; P97699;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
DE (SCA-1) (LICE) (IRP).
GN CASP3 OR CPP32.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxId=10116;
RX NM (1)
RX SEQUENCE FROM N.A.
RX MEDLINE=96358624; PubMed=8761296;
RA Juan T.S.-C., McIniece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
RA Fletcher F.A.;
RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
RT a cysteine protease resembling Interleukin-1 beta converting enzyme
RT and CED-3."
RL Oncogene 13:749-755 (1996).
RN (2)
RP SEQUENCE OF 30-241 FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=96042508; PubMed=7588240;
RA Flaws J.A., Kugu K., Trpovich A.M., Desanti A., Tilly K.I.,
RA Hirschfield A.N., Tilly J.L.;
RT "Interleukin-1 beta-converting enzyme-related proteases (IRPs) and
RT mammalian cell death: dissociation of IRP-induced oligonucleosomal
RT endonuclease activity from morphological apoptosis in granulosa cells
RT of the ovarian follicle."
RL Endocrinology 136:5042-5053 (1995).
RN (3)
RP SEQUENCE FROM N.A.

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RC TISSUE=Brain;
RX MEDLINE=97184204; PubMed=9030616;
RA Ni B., Wu X., Du Y., Su Y., Hamilton-Byrd E., Rockey P.K.,
RA Rostek P. Jr., Polter G.G., Paul S.M.;
RT "Cloning and expression of a rat brain interleukin-1beta-converting
RT enzyme (ICE)-related protease (IRP) and its possible role in
RT apoptosis of cultured cerebellar granule neurons."
RL J. Neurosci. 17:1561-1569 (1997).
RN (4)
RP SEQUENCE OF 1-264 FROM N.A.
RA Yakovlev A.G.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT
CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
CC 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROID REGULATORY
CC ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-
CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF A 17 KDA (P17) AND A 12 KDA (P12) SUBUNIT
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, LIVER, AND MUSCLE
CC BUT NOT IN KIDNEY OR TESTIS.
CC -1- DEVELOPMENTAL STAGE: HIGHLY EXPRESSED IN NEURON-ENRICHED REGIONS
CC OF THE DEVELOPING BRAIN, BUT DOWN-REGULATED TO LOW LEVELS IN THE
CC ADULT BRAIN.
CC -1- PTM: CLEAVAGE BY GRANTYME B, CASPASE-6, -8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC PROPEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 PROPEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC
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CC
CC EMBL; U49930; AAC52765.1; -
CC EMBL; U34685; AAC52261.1; -
CC EMBL; U84410; AAB41792.1; -
CC EMBL; U58656; AAB02722.1; -
CC HSSP; P42574; 1PAU.
CC MEROPS; C14.003; -.
CC InterPro; IPR002398; ICE.
CC InterPro; IPR002138; ICE_P10.
CC InterPro; IPR001309; ICE_P20.
CC Pfam; PF00655; ICE_P10; 1.
CC Pfam; PF00656; ICE_P20; 1.
CC PRINTS; PR00376; ILBENZYM.
CC SMART; SM00115; CASC; 1.
CC PROSITE; PS01122; CASPASE_CYS; 1.
CC PROSITE; PS01121; CASPASE_HIS; 1.
CC PROSITE; PS50207; CASPASE_P10; 1.
CC PROSITE; PS50208; CASPASE_P20; 1.
CC HydroLase; Thiol protease; Zymogen; Apoptosis.
CC PROPEP 1 9
CC PROPEP 10 28
CC CHAIN 29 175
CC CHAIN 176 277
CC ACT_SITE 121 121
CC ACT_SITE 163 163
CC ACT_SITE 25 29
CC CONFLICT 170 170 C -> S (IN REF. 2).
CC CONFLICT 178 178 T -> A (IN REF. 2).
CC CONFLICT 182 182 M -> V (IN REF. 2).
CC CONFLICT 187 187 I -> K (IN REF. 2).
CC CONFLICT 190 190 E -> G (IN REF. 3).

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FT CONFLICT 199 199 T -> S (IN REF. 2).
FT CONFLICT 211 211 D -> G (IN REF. 2).
FT CONFLICT 236 236 L -> I (IN REF. 4).
FT CONFLICT 245 245 T -> M (IN REF. 3).
SQ SEQUENCE 277 AA; 31491 MM; ADABF41BE2507402 CRC64;

Query Match 20.3%; Score 274; DB 1; Length 277;
Best Local Similarity 30.5%; Pred. No. 7e-14;
Matches 81; Conservative 44; Mismatches 93; Indels 48; Gaps 10;

QY 16 EERDMGARGALALVCTV-----KAREGSEVDMEALERFRYLKFEETMKRDPDTA 65
DB 34 DSSYKMYVPEGLCTIINNKNFHKSTGMSANGVDVDAANIRETFMALKYEVNRKNDLTR 93
QY 66 QQFEELEDEFOOTIDNMEPEVSCAFV-VLMAGEEGELKGEDEKVRLEDEFEVLNNNGC 124
DB 94 EIMELMD---SVSKEDSKRSSFCVYLISHGDEGVFTNGRP-VDLKULTSFFRGDYC 148
QY 125 KALRGKPRVYIIQACRGEHRDPGEELRGNEELGDEELGDEVAVLKNNPQSIPTTDTL 184
DB 149 RSLGKPRFLFIIOACRGTELDGIE---TDSGTDDWA-----CQKIPVADFL 194
QY 185 HLYTVEGYSLYRDEKSGFIQTL---TDVFIHKSGSILETEITRLMANTVMQEGK 241
DB 195 YAVSTAPGYSWRSRDSWFIQSICAMLKLYAHK---LEFMILITRV--NRKVATEFE 248
QY 242 -----PRKNPEVOSTLRKKLY 258
DB 249 SFSLDATPHAKQIPICVISMLTKELY 274

RESULT 8
ICE3 HUMAN STANDARD; PRT: 277 AA.
ID ICE3 HUMAN STANDARD; PRT: 277 AA.
AC P42574;
DT 01-NOV-1995 (Ref. 32, Created)
DT 01-NOV-1995 (Ref. 32, Last sequence update)
DT 15-JUN-2002 (Ref. 41, Last annotation update)
DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
DE (SCA-1).
GN CASP3 OR CPP32.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ALPHA AND BETA ISOFORMS).
RC TISSUE=T-cell;
RX MEDLINE=95074098; PubMed=7983002;
RA Fernandez-Alnemri T., Litwack G., Alnemri E.S.;
RT "CPP32, a novel human apoptotic protein with homology to
RT Ctenothaditis elegans cell death protein Ced-3 and mammalian
RT Interleukin-1 beta-converting enzyme.";
RL J. Biol. Chem. 269:30761-30764(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95292347; PubMed=7774019;
RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
RA Belcher D.R., Poitrier G.G., Salvesen G.S., Dixit V.M.;
RT "Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable
RT protease that cleaves the death substrate poly(ADP-ribose)
RT polymerase.";
RL Cell 81:801-809(1995).
RN [3]
RP SEQUENCE OF 29-46 AND 175-193. AND FUNCTION.
RX MEDLINE=95319529; PubMed=7596430;
RA Nicholson D.W., Ali A., Thornberry N.A., Vaillancourt J.P., Ding C.K.,
RA Gallant N., Gareau Y., Griffen P.R., Labelle M., Lazebnik Y.A.,
RA Munday D.K., Raju S.M., Smolton M.E., Yamin T.T., Li V.L.,
RA Miller D.K.;
RT "Identification and inhibition of the ICE/CED-3 protease necessary
RT for mammalian apoptosis.";

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RL Nature 376:37-43(1995).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 28-277.
RX MEDLINE=96266352; PubMed=8673606;
RA Roconda J., Nicholson D.W., Fazil K.M., Gallant M., Gareau Y.,
RA Labelle M., Peterson E.P., Rasper D.M., Ruel R., Vaillancourt J.P.,
RA Thornberry N.A., Becker J.W.;
RT "The three-dimensional structure of apoptain/CPP32, a key mediator of
RT apoptosis.";
RL Nat. Struct. Biol. 3:619-625(1996).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.
RX MEDLINE=97197830; PubMed=9045680;
RA Mitić P.R., di Marco S., Krebs J.F., Bai X., Karanewsky D.S.,
RA Priestle J.P., Tomaselli K.J., Grutter M.G.;
RT "Structure of recombinant human CPP32 in complex with the
RT tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone.";
RL J. Biol. Chem. 272:6539-6547(1997).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=20283632; PubMed=10821855;
RA Lee D., Long S.A., Adams J.L., Chan G., Vaidya K.S., Francis T.A.,
RA Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S.,
RA Levy M.A., Dewolf W.E., Jr., Keller P.M., Tomaszek T., Head M.S.,
RA Ryan M.D., Hattiwanger R.C., Liang P.-H., Janson C.A., McDevitt P.J.,
RA Johanson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,
RA Lark M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E.;
RT "Potent and selective nonpeptide inhibitors of caspases 3 and 7
RT inhibit apoptosis and maintain cell functionality.";
RL J. Biol. Chem. 275:16007-16014(2000).
RN [7]
RP PROCESSING.
RX MEDLINE=96353838; PubMed=8755496;
RA Fernandez-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
RA Wang U., Bullrich F., Fritz U.C., Trapani J.A., Tomaselli K.J.,
RA Litwack G., Alnemri E.S.;
RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RT apoptotic cysteine protease containing two FADD-like domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
RN [8]
RP CLEAVAGE OF HUNTINGTIN.
RX MEDLINE=96331285; PubMed=8696339;
RA Goldberg Y.P., Nicholson D.W., Rasper D.M., Kalchman M.A., Koide H.B.,
RA Graham R.K., Brom M., Kazemi-Esfarjani P., Thornberry N.A.,
RA Vaillancourt J.P., Hayden M.R.;
RT "Cleavage of huntingtin by apoptain, a proapoptotic cysteine protease,
RT is modulated by the polyglutamine tract.";
RL Nat. Genet. 13:442-449(1996).
RN [9]
RP FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT
PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
216-ASP-|GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATOR
ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-
HELIx LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9. INVOLVED IN THE
CLEAVAGE OF HUNTINGTIN.
RN [10]
RP ENZYME REGULATION: INHIBITED BY ISATIN SULFONAMIDES.
RN [11]
RP SUBUNIT: HETERODIMER OF A 17 kDa (p17) AND A 12 kDa (p12) SUBUNIT.
RN [12]
RP SUBCELLULAR LOCATION: Cytoplasmic.
RN [13]
RP TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SPLEEN, HEART, LIVER
AND KIDNEY. MODERATE LEVELS IN BRAIN AND SKELETAL MUSCLE, AND LOW
IN TESTIS. ALSO FOUND IN MANY CELL LINES, HIGHEST EXPRESSION IN
CELLS OF THE IMMUNE SYSTEM.
RN [14]
RP PTM: CLEAVAGE BY GRANZYME B, ARAF-1, CASPASE-6, -8 AND -10
GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE
PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE
ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT
OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
AND VICE VERSA.
RN [15]
RP SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
RN [16]
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DR EMBL; U13737; AAA65015.1; -
 DR EMBL; U13738; AAA60355.1; -
 DR EMBL; U26943; AAA74929.1; -
 DR PDB; 1PAU; 07-JUL-97.
 DR PDB; 1CE3; 24-DEC-97.
 DR PDB; 1GFW; 23-JUN-00.
 DR MEROPS; C14.003; -
 DR Genew; HGNC:1504; CASP3.
 DR MIM; 600636; -
 DR InterPro; IPR002398; ICE_P10.
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P10.
 DR Pfam; PF00655; ICE_P10; 1.
 DR Pfam; PF00656; ICE_P20; 1.
 DR PRINTS; PR00376; IL1BCENZYM.
 DR SMART; SMO0115; CASc; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR HydroLase; Thiol protease; Zymogen; Apoptosis; Polymorphism;
 KM 3D-structure. 1
 FT PROPEP 1 9
 FT CHAIN 28
 FT CHAIN 29 175 APOPAIN P12 SUBUNIT.
 FT ACT_SITE 176 277 APOPAIN P12 SUBUNIT.
 FT ACT_SITE 121 121 BY SIMILARITY.
 FT ACT_SITE 163 163 BY SIMILARITY.
 FT VARIANT 190 190 D -> E (IN ISOFORM BETA).
 FT VARIANT /FTID=VAR_001401.
 SQ SEQUENCE 277 AA; 31594 MW; 8E34DD2ACE6EF64B CRC64;

Query Match 20.2%; Score 273; DB 1; Length 277;
 Best Local Similarity 31.5%; Pred. No. 8,4e-14;
 Matches 86; Conservative 41; Mismatches 104; Indels 42; Gaps 10;

QY 6 SEMSDPOLQOEERYDMGARGALALTLCTVTR-----ARCGSEVDMALRRMRPLK 55
 DB 24 SSMSSGSLDMSYKMDYPMGCLITNNKNFHKSTGMSRSTGTDVANLSTFNNLKY 83
 QY 56 ESTMKRDPAAQOFLBELDFOOTIDNMEEPVSCAFV-VLMHGEBSGLKGEDEKVRLED 114
 DB 84 EVRNKNDLTR---BEIVELMRDVSKEHDSKRSFVCVLLSHGEEGIIPTGTGP-VDLKK 138
 QY 115 LFEVLNNKCKALRGKPKYIIQACGHRDPGEELRGNEELGGDELDGDEFAVLKNNP 174
 DB 139 IINFRGDRCRSLTGKPKLFIQACRGTLDCGIE---TDSGVD---DDMACKH--- 186
 QY 175 OSIPTVDTLHYSTVEGYLSYRHDEKSGFIQTLTDFVHHKSGSLLELTETRIIMANT 234
 DB 167 --IPVDADLVYSTAPGYYSWRNSKDSMFTQSLC-AMLKQYADLFTMHILTRY--NR 241
 QY 235 EVMQEGK-----PRVNPVOSTLRKKLY 258
 DB 242 KVATEFESFSFDATFPAKKQIPCIIVSMLTKELY 274

RESULT 9
 ICE3_CRIL0 STANDARD; PRT; 277 AA.
 ID ICE3_CRIL0
 AC Q60431;
 DT 01-NOV-1997 (Rel. 35, Last Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Aopain precursor (EC 3.4.22.-) (Cysteine protease CP32) (Yama
 DE protein) (CP-32) (Caspase-3) (SREBP cleavage activity 1)
 DE (SCA-1).

GN CASP3 OR CP32.
 OS Cricetus longicaudatus (long-tailed hamster) (Chinese hamster).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetus.
 NC NCB1_TaxID=10030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RC MEDLINE=96183185; PubMed=8605870.
 RA Wang X., Zelemski N.G., Yang J., Sakai J., Brown M.S.,
 RA Goldstein J.L.;
 RT "Cleavage of sterol regulatory element binding proteins (SREBPs) by
 RT CP32 during apoptosis.";
 RL EMBO J. 15:1012-1020 (1996).

CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT
 CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
 CC 216-ASP-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY
 CC ELEMENT BINDING PROTEINS (SREBPs) BETWEEN THE BASIC HELIX-LOOP-
 CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
 CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).
 CC -1- SUBUNIT: HETERODIMER OF A 17 KDA (P17) AND A 12 KDA (P12) SUBUNIT
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CP32 ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.

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DR EMBL; U27463; AAA01511.1; -
 DR HSSP; P42574; 1PAU.
 DR MEROPS; C14.003; -
 DR InterPro; IPR002398; ICE_P10.
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR Pfam; PF00655; ICE_P10; 1.
 DR Pfam; PF00656; ICE_P20; 1.
 DR PRINTS; PR00376; IL1BCENZYM.
 DR SMART; SMO0115; CASc; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 KM HydroLase; Thiol protease; Zymogen; Apoptosis.
 FT PROPEP 1 9
 FT CHAIN 28
 FT CHAIN 29 175 APOPAIN P12 SUBUNIT.
 FT ACT_SITE 176 277 APOPAIN P12 SUBUNIT.
 FT ACT_SITE 121 121 BY SIMILARITY.
 FT ACT_SITE 163 163 BY SIMILARITY.
 SQ SEQUENCE 277 AA; 31612 MW; 0BF3A4590A2828A3 CRC64;

Query Match 19.5%; Score 263; DB 1; Length 277;
 Best Local Similarity 33.1%; Pred. No. 4,8e-13;
 Matches 78; Conservative 35; Mismatches 85; Indels 38; Gaps 9;

QY 36 RRGSEVDMALERMRYLKFESTMKRDPTAAQOFLBELDFOOTIDNMEEPVSCAFV-VLM 94
 DB 64 RSGTVDVDAKRLKETFMALKEVRNNKNDLTR---BEIVELNNKASKHDSKRSFVCVIL 119
 QY 95 AHGEGLLKGEDEKVRLEDLFEVLNNKCKALRGKPKYIIQACGHRDPGEELRGNE 154


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Db 120 SHGEGVIFGIDGP-IDLKLTYSFRGDYCRSLGKPKLFIQACRGELDCGIETSGT 178
Qy 155 ELGDEELGGDEVALKNPNOSIPTYDTLHIVSTVEGYSYRHDGSGFIQITLD--- 211
Db 179 E-----DDMTC-----OKTVEADFLYASTAPRYSWRNPKGSGWITQSLCSMLK 224
Qy 212 VFIHKGSILEETETRLMANTEVMOEGK-----PRKNPEVOSTLRKLY 258
Db 225 LVAMK-----LEPMILTRV--NRKVATEFESFLSDTFHAKQIPCIYVMTKELY 274

RESULT 10
CED3 CAEVU STANDARD; PRT; 496 AA.
ID CED3 CAEVU AC P45436;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cell death protein 3 precursor (EC 3.4.22.-).
GN CED-3.
OS Caenorhabditis vulgaria.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=31233;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94061982; PubMed=8242740;
RA Yuan J., Shaham S., Ledoux S., Ellis H.M., Horvitz H.R.;
RT "The C. elegans cell death gene ced-3 encodes a protein similar to
RT mammalian interleukin-1 beta-converting enzyme."
RL Cell 75:641-652(1993).
CC -1- FUNCTION: ACTS AS A CYSTEINE PROTEASE IN CONTROLLING PROGRAMMED
CC CELL DEATH BY PROAPOPTOTICALLY ACTIVATING OR INACTIVATING A
CC SUBSTRATE PROTEIN OR PROTEINS, A POTENTIAL SUBSTRATE MAY BE CED-4.
CC ALTERNATIVELY IT MIGHT DIRECTLY CAUSE CELL DEATH BY
CC PROAPOPTOTICALLY CLEAVING PROTEINS THAT ARE CRUCIAL FOR CELL
CC VIABILITY (BY SIMILARITY).
CC -1- SUBUNIT: COULD BE A HETERODIMER OF TWO SUBUNITS DERIVED FROM THE
CC PRECURSOR SEQUENCE BY A PROBABLE AUTOCATALYTIC MECHANISM.
CC -1- PTM: MAY BE REGULATED BY PHOSPHORYLATION.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC HSSP: P42574; ICP3.
DR HSSP: C14_002; -.
DR INTERPRO: IPR001315; CARD.
DR INTERPRO: IPR002398; ICE.
DR INTERPRO: IPR002138; ICE_p10.
DR INTERPRO: IPR001309; ICE_p20.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00655; ICE_p10; 1.
DR Pfam: PF00656; ICE_p20; 1.
DR PRINTS: PR00376; ILICENZIME.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00115; CASC; 1.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis; Phosphorylation.
FT CHAIN 1 364 CELL DEATH PROTEIN 3 SUBUNIT 1
FT CHAIN 1 364 (POTENTIAL).
FT CHAIN 365 496 CELL DEATH PROTEIN 3 SUBUNIT 2
FT CHAIN 1 91 (POTENTIAL).
FT DOMAIN 1 91 CARD.
FT ACT_SITE 308 308 BY SIMILARITY.
FT ACT_SITE 351 351 BY SIMILARITY.
SQ SEQUENCE 496 AA; 55945 MW; 58E73C790DC3BD38 CRC64;

Query Match 19.2%; Score 259.5; DB 1; Length 496;
Best Local Similarity 29.5%; Pred. No. 1.ee-12;
Matches 70; Conservative 52; Mismatches 96; Indels 19; Gaps 8;

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Qy 36 REGSEVMEALERMFRYLKEESTKRDPTAQOFLSEELDEFQOTIDNMEEPVSCAFVIMA 95
Db 253 RNTGKADKXDLTNIFRCMGV-TVIKCNISGRGLTTRDAKN-----ETGDSALIVILS 307
Qy 96 HGEELGLKGEDEKVRLEDFEVLYNNKCALNGKPKVYIIOACRGEHDPG---EELR 151
Db 308 HGEENVIVIGVDVSVNHEIYDILLNANAPRLANKPYLVEVQACRGERRDNGFPVLDSDV 367
Qy 152 GNEEL---GGDEELGGDEVALKNPNOSI---PTYDTLHIVSTVEGYSYRHDGSG 204
Db 368 GVPSLIRRGWMDNRGPFILCVBPQAOVWRKKPSQADILIRVATTVAQVYSWRNSAGSW 427
Qy 205 FIQTLTDFV-IHKKG-SILEETETRLMA-NTVEVMOEGKPRKNPEVOSTLRKLY 258
Db 428 FIQVCEVFSTHAKDMVVELLTVENKVKVACGFTSGANILKQMPMTSLKKPF 484

RESULT 11
ICE7 HUMAN STANDARD; PRT; 303 AA.
ID ICE7 HUMAN AC P55210; O13364; Q96BA0;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (ICE-1-like apoptotic protease 3)
DE (ICE-LAP3) (Apoptotic protease Mch-3) (CWH-1).
GN CASP7 OR MCH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ALPHA ISOFORM).
RX MEDLINE=96139498; PubMed=8576161;
RA Duan H., Chinnaiyan A.M., Hudson P.L., Wing J.P., He W.-W.,
RA Dixit V.M.;
RT "ICE-LAP3, a novel mammalian homologue of the Caenorhabditis elegans
RT cell death protein Ced-3 is activated during Fas- and tumor necrosis
RT factor-induced apoptosis."
RL J. Biol. Chem. 271:1621-1625(1996).
RN [2]
RP SEQUENCE FROM N.A. (ALPHA ISOFORM).
RC TISSUE=Spleen;
RX MEDLINE=96147144; PubMed=8567622;
RA Lipke J.A., Gu Y., Sarnacki C., Caron P.R., Su M.S.-S.;
RT "Identification and characterization of CPP32/Mch2 homolog 1, a novel
RT cysteine protease similar to CPP32."
RL J. Biol. Chem. 271:1825-1828(1996).
RN [3]
RP SEQUENCE FROM N.A. (ALPHA AND BETA ISOFORMS).
RC TISSUE=T-cell;
RX MEDLINE=96105019; PubMed=8521391;
RA Fernandes-Alnemri T., Takahashi A., Armstrong R.C., Krebs J.,
RA Fritz L.C., Tomaselli K.J., Wang L., Yu Z., Croce C.M., Salveson G.,
RA Barnhaw W.C., Litwack G., Alnemri E.S.;
RT "Wch3, a novel human apoptotic cysteine protease highly related to
RT CPP32."
RL Cancer Res. 55:6045-6052(1995).
RN [4]
RP SEQUENCE FROM N.A. (ALPHA AND ALPHA' ISOFORMS).
RC TISSUE=Fetal lung, and fetal spleen;
RX MEDLINE=97224489; PubMed=9070923;
RA Juan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Fletcher F.A.;
RT "Identification and mapping of Casp7, a cysteine protease resembling
RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3."
RL Genome 40:86-93(1997).
RN [5]
RP SEQUENCE FROM N.A. (ALPHA ISOFORM).
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

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RN [6]
 RX MEDLINE=96353838; PubMed=8755496;
 RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
 RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomasselli K.J.,
 RA Litwack G., Alnemri E.S.;
 RT "In vitro activation of CPP32 and Mch3 by Mch3, a novel human
 RT apoptotic cysteine protease containing two FAD-like domains";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
 CC -FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL
 CC REGULATORY ELEMENT BINDING PROTEINS (SREBPS). PROTEOLYTICALLY
 CC CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-|-GLY-217
 CC BOND. OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH.
 CC -ENZYME REGULATION: INHIBITED BY ISATIN SULFONAMIDES.
 CC -SUBUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT.
 CC -SUBCELLULAR LOCATION: Cytoplasmic.
 CC -ALTERNATIVE PRODUCTS: 3 ISOFORMS; ALPHA (SHOWN HERE), BETA AND
 CC ALPHA'; ARE PRODUCED BY ALTERNATIVE SPLICING. THE BETA ISOFORM IS
 CC NOT PROTEOLYTICALLY ACTIVE.
 CC -TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SKELETAL MUSCLE,
 CC LIVER, KIDNEY, SPLEEN AND HEART, AND MODERATELY IN TESTIS. NO
 CC EXPRESSION IN THE BRAIN.
 CC -PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
 CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
 CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
 CC VICE VERSA.
 CC -SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -CAUTION: WHAT WE CALL ALPHA' ISOFORM IS KNOWN IN REF. 4 AS BETA.
 CC BUT AS BETA IS ALREADY DEFINED IN REF. 3 WE HAVE CALLED IT ALPHA'.
 CC -----
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 CC -----
 CC EMBL; U39613; AAC50346.1; -
 CC EMBL; U40281; AAC50352.1; -
 CC EMBL; U37448; AAC50303.1; -
 CC EMBL; U37449; AAC50304.1; -
 CC EMBL; U67319; AAC51152.1; -
 CC EMBL; U67320; AAC51153.1; -
 CC EMBL; U67206; AAF21460.1; -
 CC EMBL; BC015799; AAH15799.1; -
 CC HSSP; P42574; 1PAU.
 CC MEROPS; C14.004; -
 CC Genew: HGNC:1508; CASP7.
 CC MIM; 601761; -
 CC InterPro; IPR002398; ICE.
 CC InterPro; IPR002138; ICE_P10.
 CC InterPro; IPR001309; ICE_P20.
 CC Pfam; PF00655; ICE_P10; 1.
 CC Pfam; PF00656; ICE_P20; 1.
 CC PRINTS; PR00376; ILBCENZYM.
 CC SMART; SMO0115; CASC; 1.
 CC PROSITE; PS01122; CASPASE_CYS; 1.
 CC PROSITE; PS01121; CASPASE_HIS; 1.
 CC PROSITE; PS02027; CASPASE_P10; 1.
 CC PROSITE; PS02028; CASPASE_P20; 1.
 CC Hydrolase; Thiol protease; Zymogen; Apoptosis; Alternative splicing.
 FT PROPEP 1 23
 FT CHAIN 24 198 CASPASE-7 SUBUNIT P20.
 FT PROPEP 199 206
 FT CHAIN 207 303 CASPASE-7 SUBUNIT P11.
 FT ACT_SITE 144 144 BY SIMILARITY.
 FT ACT_SITE 186 186
 FT VARSPLIC 1 1 M -> MDCVGPMPGKMKHLKNTSCGSSGICASYVTOM
 FT VARSPLIC 149 303 (IN ISOFORM ALPHA').
 FT VARSPLIC VIYKDGVTPIKDLTAHFRGDRCKTLLEKPKLFIQACRG

FT ELDLDGIQADSGPIINDTDANPRYKIPVEADFLFASTVTVGY
 FT SWRSRGSMFVQALCSILIEHGKDLLEIHOILTRVDRAR
 FT HFEQSDDPHFEKQIPCVSMILTELYFSQ -> MESCS
 FT VTQAGVQRDLGRLQPPPLPAAGPSILMAASRTPRSPMTQ
 FT MLIDTRSGWKLTSSSPIPFPOAIRGAGOEAPGCKPSA
 FT PSWRSTKTMKSCRSSRG (IN ISOFORM BETA).
 FT C->A: NO APOPTOTIC ACTIVITY.
 FT D -> E (IN REF. 5).
 FT G -> A (IN REF. 1).
 SQ SEQUENCE 303 AA; 34276 MW; CD373EE54A232CA4 CRC64;
 Query Match 18.9%; Score 255.5; DB 1; Length 303;
 Best Local Similarity 30.5%; Pred. No. 2e-12;
 Matches 80; Conservative 41; Mismatches 100; Indels 41; Gaps 10;
 QY 18 RYDMSGARLALTLCTV-----AREGEYDMALERMFRYLKFESTMKRPTA-- 65
 DB 59 QYNNMFEKLGKCIINNNKPFKVTGMGRNCTDADALFRCFSSLSFDVIVYNDSCAK 118
 QY 66 -QOFLKEIDFQOQTIIDWEEBVSQAFVYLVMAHGEGLKDEKXVRLDLFEVLNNKNC 124
 DB 119 MQDLKKASEEDHT-----NAACFACILSHGSENYIGKD-GVTPDKDLTAHFRGDR 171
 QY 125 KALGKPKVYIIQCRGEHRDPGEELAGNEELGDEGLGDEVAVLKNPQ-SIPTYDPT 183
 DB 172 KTLLEKPKLFIQACRGTELDG-----IQADSGPIINDTD---NPKYKIPVEADP 219
 QY 184 LHIYSTVEGYLSYRHDEKSGFIQTLTDVFIHKKGSILLETETRL---MANTVMOEG 240
 DB 220 LFAYSTVGYISWMSPRGSMFVQALCSI-LEHNGKOLEIQLTRVNDVRAHFEQSD 278
 QY 241 KP---RKVNEVOSTLRKKLY 258
 DB 279 DPHFEKQIPCVSMILTKELY 300
 RESULT 12
 ICED7 MOUSE STANDARD; PRT; 303 AA.
 AC P97864; 008669;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Caspase-7 precursor (EC 3.4.22.-) (LICE2 cysteine protease) (Apoptotic
 DE protease Mch-3).
 GN CASP7 OR MCH3 OR LICE2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=97224489; PubMed=9070923;
 RA Juan T.S.-C., McIntee I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
 RA Copeland N.G., Fletcher F.A.;
 RT "Identification and mapping of Casp7, a cysteine protease resembling
 RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3.";
 RL Genomics 40:86-93(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97190206; PubMed=9038361;
 RA Mukasa T., Khoroqui Y., Tsukahara T., Momoi M.Y., Kimura I.,
 RA Momoi T.;
 RT "Mortaminin enhances CPP32-like activity during neuronal
 RT differentiation of P19 embryonal carcinoma cells induced by retinoic
 RT acid.";
 RL Biochem. Biophys. Res. Commun. 232:192-197(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/An;
 RX MEDLINE=97190206; PubMed=9038361;
 RA van de Creen M., Vandenberghe P., Declercq W., van den Brande I.,

RA van Loo G., Molemans F., Schotte P., van Criekeing W., Beyaert R.,
 RA Fiers W.,
 RT "Characterization of seven murine caspase family members."
 RL FEBS Lett. 403:61-69(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Strauberg R.,
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION, CLEAVES AND ACTIVATES STEROL
 CC REGULATORY ELEMENT BINDING PROTEIN (SERPS). OVEREXPRESSION
 CC PROMOTES PROGRAMMED CELL DEATH (BY SIMILARITY).
 CC -1- SUBUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, LUNG, LIVER, AND
 CC KIDNEY. LOW LEVELS IN SPLEEN, SKELETAL MUSCLE, AND TESTIS. NO
 CC EXPRESSION IN THE BRAIN.
 CC -1- PTM: CLEAVAGES BY GRAVITIME B OR CASPASE-10 GENERATE THE TWO ACTIVE
 CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
 CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -----
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 CC -----
 CC EMBL: U67321; AAC53068.1; ALT_INIT.
 CC EMBL: D86353; BA19730.1; -
 CC EMBL: Y13088; CA73530.1; -
 CC EMBL: BC005428; AAH05428.1; -
 CC HSSP: P42574; 1PAU.
 CC MEROPS: C14.004; -
 CC MGD: MGI:109383; Casp7.
 CC InterPro: IPR002398; ICE.
 CC InterPro: IPR002138; ICE_P10.
 CC InterPro: IPR001309; ICE_P20.
 CC Pfam: PF00655; ICE_P10; 1.
 CC Pfam: PF00656; ICE_P20; 1.
 CC PRINTS: PRO0376; ILJBCENZME.
 CC SMART: SM00115; CASC; 1.
 CC PROSITE: PS01122; CASPASE_CYS; 1.
 CC PROSITE: PS01121; CASPASE_HIS; 1.
 CC PROSITE: PS50207; CASPASE_P10; 1.
 CC PROSITE: PS50208; CASPASE_P20; 1.
 CC HydroLase: Thiol protease; Zymogen; Apoptosis.
 CC PROPER 1 23 BY SIMILARITY.
 CC CHAIN 24 198 CASPASE-7 SUBUNIT P20 (BY SIMILARITY).
 CC PROPEP 199 206 BY SIMILARITY.
 CC CHAIN 207 303 CASPASE-7 SUBUNIT P11 (BY SIMILARITY).
 CC ACT SITE 144 144 BY SIMILARITY.
 CC ACT SITE 186 186 BY SIMILARITY.
 CC CONFLICT 10 11 EL -> DW (IN REF. 2).
 CC CONFLICT 45 45 A -> T (IN REF. 2).
 CC CONFLICT 48 49 VR -> RQ (IN REF. 2).
 CC SEQUENCE 303 AA; 34060 MW; 747787B5BDE5F744 CRC64;
 Query Match 18.9%; Score 254.5; DB 1; Length 303;
 Best Local Similarity 32.5%; Pred. No. 2.4e-12;
 Matches 76; Conservative 37; Mismatches 90; Indels 31; Gaps 8;

QY 153 NEBIGDEELGGEVAVLKNPPOS-IPYTDLHIYSTVEGYLSYRDEKSGSFIQTLD 211
 Db 195 -----IQADSGPINDIDANPNRKIVPEADPLFAVSTVGYGSMRPGKSGMFWQLCS 247
 QY 212 VFHKKGSITLLEIEIRL--MANTVMEQGRKPR----KVPNVOSTLTKKLY 258
 Db 248 I-DNEHGKDEIMQILTRVNDVARHFPESQDDPRFNEKQIDPCWVSMLTRKELY 300
 RESULT 13
 ID CED3_CAEEL STANDARD; PRT; 503 AA.
 AC P42573; P45435; O9NAC8;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cell death protein 3 precursor (EC 3.4.22.-).
 GN CED-3 OR C48D1.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS.
 RP STRAIN=Bristol N2;
 RX MEDLINE=94061982; PubMed=8242740;
 RA "Van J., Shaham S., Ledoux S., Ellis H.M., Horvitz H.R.,
 RT "The C. elegans cell death gene ced-3 encodes a protein similar to
 RT mammalian Interleukin-1 beta-converting enzyme".
 RL Cell 75:641-652(1993).
 RN [2]
 RP REVISION TO 418.
 RA Horvitz H.R.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RP STRAIN=Bristol N2;
 RA Burton J.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP REVISIONS.
 RA Durbin R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ACTS AS A CYSTEINE PROTEASE IN CONTROLLING PROGRAMMED
 CC CELL DEATH BY PROTEOLYTICALLY ACTIVATING OR INACTIVATING A
 CC SUBSTRATE PROTEIN OR PROTEINS, A POTENTIAL SUBSTRATE MAY BE CED-4.
 CC ALTERNATIVELY IT MIGHT DIRECTLY CAUSE CELL DEATH BY
 CC PROTEOLYTICALLY CLEAVING PROTEINS THAT ARE CRUCIAL FOR CELL
 CC VIABILITY.
 CC -1- SUBUNIT: COULD BE A HETERODIMER OF TWO SUBUNITS DERIVED FROM THE
 CC PRECURSOR SEQUENCE BY A PROBABLE AUTOCATALYTIC MECHANISM.
 CC -1- DEVELOPMENTAL STAGE: MOST ABUNDANT DURING EMBRYOGENESIS AND IS
 CC ALSO DETECTED AT LATER STAGES.
 CC -1- PTM: MAY BE REGULATED BY PHOSPHORYLATION.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
 CC -----
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 CC -----
 CC EMBL: L29052; AA27982.2; -
 CC EMBL: AF210702; AAG42045.1; -
 CC EMBL: Z81049; CAB61001.2; -
 CC WormPep; C48D1.2; CE29088.
 CC HSSP: P42574; 1CP3.
 CC MEROPS: C14.002; -
 CC InterPro: IPR001315; CARD.

DR InterPro; IPR002398; ICE.
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00655; ICE_P10; 1.
 DR Pfam; PF00656; ICE_P20; 1.
 DR PRINTS; PR00376; ILICENZYME.
 DR SMART; SM00114; CARD; 1.
 DR SMART; SM00115; CASc; 1.
 DR PROSITE; PS50209; CARD; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 KW Hydrolyase; Thiol protease; zymogen; Apoptosis; Phosphorylation.
 FT CHAIN 1 371
 FT CHAIN 372 503
 FT DOMAIN 1 91
 FT ACT_SITE 107 205
 FT ACT_SITE 304 304
 FT ACT_SITE 358 358
 FT MUTAGEN 27 27
 FT MUTAGEN 65 65
 FT MUTAGEN 360 360
 FT MUTAGEN 449 449
 FT MUTAGEN 466 466
 FT MUTAGEN 483 483
 FT MUTAGEN 486 486
 SQ SEQUENCE 503 AA; 56616 MW; 722D5831F94DMA69 CRC64;

Query March 18.7%; Score 253; DB 1; Length 503;
 Best Local Similarity 28.9%; Pred. No. 5.8e-12;
 Matches 69; Conservative 49; Mismatches 101; Indels 20; Gaps 7;

QY 36 REGSEVMEALERMFRYLKFESESTMKRDPTAQCFLBELDFEFOOTIINWEEPVSCAFVILMA 95
 DB 259 RRGCTADKDNLTNLRFCMGVYICKDNLTGRMLTIRPAK---HEHSGSALLVILS 314
 QY 96 HGEELKGEDEKMYRLDFEVLNNKCKALKRKRYIIACGEGHRDPGEELRGNEE 155
 DB 315 HGEENVIIIGVDIPISTHEIYDLNNAANAPRLANKKIVFVACGERDNGFPVLDSVD 374
 QY 156 -----LGGDEELG--DEVAVLNKNPQSI-----PTVDTLHISTVSGYSYHDEMG 202
 DB 375 GVPARLRGMWRDRLPFLFGLGCVRPQVQVWRKRPQADILIAVATTAQVSWRNSARG 434
 QY 203 SGFIOTLTVDF-IHKKG-SILELTERITRLMA-NTEVMQEGKPRKVPVQSTLRKLY 258
 DB 435 SWFIQAVCEVFSTHAKDMVVELLTVNKKVACGFGTSGSNILKQMPERTSLKKFY 493

RESULT 14

ICE9_HUMAN STANDARD. PRT: 416 AA.
 AC P55211.Q82852.095348.Q9U108.Q9UE03;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Caspase-9 precursor (EC 3.4.22.-) (CASP-9) (ICE-like apoptotic
 DE protease 6) (ICE-LAP6) (Apoptotic protease Mch-6) (Apoptotic protease
 DE activating factor 3) (APAF-3).
 GN CASP9 OR MCH6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96279246; PubMed=8663294;
 RA Duan H., Orth K., Chinnaiyan A.M., Poirier G.G., Froelich C.J.,
 RA He W.-W., Dixit V.M.;

RT "ICE-LAP6, a novel member of the ICE/Ced-3 gene family, is activated
 RT by the cytotoxic T cell protease granzyme B.";
 RL J. Biol. Chem. 271:16720-16724(1996).
 RN [2]
 RP SEQUENCE FROM N.A. AND PROCESSING.
 RC TISSUE=T-cell;
 RX MEDLINE=97059171; PubMed=8900201;
 RA Srinivasula S.M., Fernandes-Alnemri T., Zangrilli J., Robertson N.,
 RA Armstrong R.C., Wang L., Trapani J.A., Tomaselli K.J., Litwack G.,
 RA Alnemri E.S.;
 RT "The Ced-3/interleukin 1beta converting enzyme-like homolog Mch6 and
 RT the lamin-cleaving enzyme Mch2alpha are substrates for the apoptotic
 RT mediator CPP32.";
 RL J. Biol. Chem. 271:27099-27106(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99315341; PubMed=10384055;
 RA Hadano S., Nasir J., Nichol K., Raepers D.M., Vailancourt J.P.,
 RA Sherer S.W., Beatty B.G., Ikeda J.E., Nicholson D.W., Hayden M.R.;
 RT "Genomic organization of the human caspase-9 gene on chromosome
 RT 1p36.1-p36.3.";
 RL Mamm. Genome 10:757-760(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).
 RX MEDLINE=99168502; PubMed=10070954;
 RA Srinivasula S.M., Ahmed M., Guo Y., Zhan Y., Lazebnik Y.,
 RA Fernandes-Alnemri T., Alnemri E.S.;
 RT "Identification of an endogenous dominant-negative short isoform of
 RT caspase-9 that can regulate apoptosis.";
 RL Cancer Res. 59:999-1002(1999).
 RN [5]
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).
 RC TISSUE=Stomach cancer;
 RA Izawa M., Mori T., Ito H., Saitenji T.;
 RT "Molecular cloning and sequencing of a cDNA predicting an alternative
 RT form of pro-caspase-9 from human gastric cancer cell lines.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).
 RA Mino Y., Momoi T., Fujita E.;
 RT "A novel splicing product of human caspase-9 lacking protease
 RT activity.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).
 RX MEDLINE=99107856; PubMed=9890966;
 RA Seol D.W., Billiar T.R.;
 RT "A caspase-9 variant missing the catalytic site is an endogenous
 RT inhibitor of apoptosis.";
 RL J. Biol. Chem. 274:2072-2076(1999).
 CC -I- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC 1 LEADS TO ACTIVATION OF THE PROTEASE WHICH THEN CLEAVES AND
 CC ACTIVATES CASPASE-3. PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE)
 CC POLYMERASE (PARP).
 CC -I- FUNCTION: THE SHORT ISOFORM LACKS ACTIVITY IS AN DOMINANT-NEGATIVE
 CC INHIBITOR OF CASPASE-9.
 CC -I- SUBUNIT: Heterodimer of a 35 kDa (P35) and a 10 kDa (P10) subunit.
 CC Caspase-9 and APAF1 bind to each other via their respective NH2-
 CC terminal CED-3 homologous domains in the presence of cytochrome C
 CC and ATP. Interacts with BIRC7.
 CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG/9L/ALPHA FORM (SHOWN
 CC HERE) AND A SHORT/9S/BETA FORM; ARE EXPRESSED BY ALTERNATIVE
 CC SPLICING.
 CC -I- TISSUE SPECIFICITY: UBIQUITOUS, WITH HIGHEST EXPRESSION IN THE
 CC HEART, MODERATE EXPRESSION IN LIVER, SKELETAL MUSCLE, AND
 CC PANCREAS. LOW LEVELS IN ALL OTHER TISSUES.
 CC -I- PTM: CLEAVAGES AT ASP-315 BY GRANZYME B AND AT ASP-330 BY CPP32
 CC GENERATE THE TWO ACTIVE SUBUNITS. CASPASE-8 AND -10 CAN ALSO BE
 CC INVOLVED IN THESE PROCESSING EVENTS.
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -I- SIMILARITY: CONTAINS 1 CARD DOMAIN.

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DR EMBL; U65390; AAC50640.1; -;
DR EMBL; U60521; AAC50776.1; -;
DR EMBL; AB019305; BAA82697.1; -;
DR EMBL; AB019197; BAA82697.1; JOINED.
DR EMBL; AB019198; BAA82697.1; JOINED.
DR EMBL; AB019199; BAA82697.1; JOINED.
DR EMBL; AB019200; BAA82697.1; JOINED.
DR EMBL; AB019201; BAA82697.1; JOINED.
DR EMBL; AB019202; BAA82697.1; JOINED.
DR EMBL; AB019203; BAA82697.1; JOINED.
DR EMBL; AB019204; BAA82697.1; JOINED.
DR EMBL; AF093130; AAD12248.1; -;
DR EMBL; AB015653; BAA78780.1; -;
DR EMBL; AB020979; BAA87905.1; -;
DR EMBL; AF110376; AAD13615.1; -;
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.010; -;
DR Genew; HGNC:1511; CASP9.
DR MIM; 602234; -;
DR InterPro; IPR003315; CARD.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00655; ICE_P10; 1.
DR Pfam; PF00656; ICE_P20; 1.
DR PRINTS; PR00376; IILBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR Hydrobase; Thiol protease; zymogen; Apoptosis; Alternative splicing.
KW PROPEP 1 ?
FT CHAIN ? 315 CASPASE-9 SUBUNIT P35.
FT PROPEP 316 330
FT CHAIN 331 416 CASPASE-9 SUBUNIT P10.
FT DOMAIN 1 92
FT ACT_SITE 237 237 CARD.
FT ACT_SITE 287 287 BY SIMILARITY.
FT VARSPIC 140 289 MISSING (IN SHORT ISOFORM).
FT CONFLICT 28 28 A -> V (IN REF. 1 AND 7).
FT CONFLICT 32 32 S -> R (IN REF. 1, 4, 5 AND 7).
FT CONFLICT 96 96 A -> G (IN REF. 1).
FT CONFLICT 197 197 P -> L (IN REF. 1).
FT CONFLICT 221 221 Q -> R (IN REF. 1).
SQ SEQUENCE 416 AA; 46195 MM; 874830P17F8DC4CD CRC64;

Query Match 18.5%; Score 250; DB 1; Length 416;
Best Local Similarity 29.1%; Pred. No. 7,7e-12;
Matches 74; Conservative 46; Mismatches 90; Indels 44; Gaps 8;

QY 34 KARGSEVDMALRMPFYLFKESFMKRPDPTAQQGLELDFOQTIDWMEBPVSCAPVYL 93
DB 178 RTTGSNIDCKLRRRSSPFHWEVKDDLTKKKVLLALLEAODHG--ALDCVVVI 234
QY 94 MANGE-----GLKGEDEKVRLELDLFEVLNNKNCALRGKPKYIIOACRGEHRDP 146
DB 235 LSHCQASHLQFPAGVYCTDGCPSVVEKIVNIPGTSFSLGGRKPLFFIACGEGEKDH 294
QY 147 GEELRGNEBELGDELDGEDEVAVLNKDP-----SIPTYTDTLHI 186
DB 295 GFEVASTSP--EDESP-----SNRPDPATFOEGLRTFDOLAISLPTSDIFVS 344

QY 187 YSTVEGLSYRHDKSGFIQTLDFVHHKGSILEETIRLMANTEWQEGPKRVN 246
DB 345 YSTPGVSWMDPRDSSGWYETTLDIR--EQMAHSEDLQSLLVANA-VSKGIYKQM- 400
QY 247 PEVOSTLRKKLYLQ 260
DB 401 PGCFNPLRKKLFK 414

RESULT 15
ID7_MESAU STANDARD; PRT; 303 AA.
AC P55214;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-7 precursor (BC 3.4.22.-) (ICE-1-like apoptotic protease 3)
DE (ICE-LAP3) (Apoptotic protease Mch-3) (SREBP cleavage activity 2)
DE (SCA-2).
GN CASP7 OR MCH3.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC STRAIN=Syrian; TISSUE=Liver;
RX MEDLINE=96224303; PubMed=8643593;
RA Pal J.-T., Brown M.S., Goldstein J.L.;
RT "Purification and cDNA cloning of a second apoptosis-related cysteine
RT protease that cleaves and activates sterol regulatory element binding
RL proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:5437-5442(1996).
CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL
CC REGULATORY ELEMENT BINDING PROTEIN (SREBP). PROTEOLYTICALLY
CC CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-[GLY-217
CC BOND. OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH (BY
CC SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
CC SUBUNIT. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -----
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KM Hydrolase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 23
FT CHAIN 24 198 CASPASE-7 SUBUNIT P20.
FT PROPEP 199 206 BY SIMILARITY.
FT CHAIN 207 303 CASPASE-7 SUBUNIT P11.
FT ACT_SITE 144 144 BY SIMILARITY.
FT ACT_SITE 186 186 BY SIMILARITY.
SQ SEQUENCE 303 AA; 34037 MW; EA29356D90984648 CRC64;

Query Match 18.5%; Score 249.5; DB 1; Length 303;
Best Local Similarity 32.2%; Pred. No. 5.7e-12;
Matches 76; Conservative 36; Mismatches 89; Indels 35; Gaps 9;

QY 36 REGSEVDMLEALERMFRYLKFESTMKRDPTA---QQFLBELDEFQQTIDNWEEPVSCAFVY 92
DB 87 RNGTHDKDAEALFKCFRSLGFDVVVYNDSCAMQDLRKASEDHNS-----ACFACV 140
QY 93 LMAHGEGLLNKGEDEKMWRLBDLFEVLNNKNCALRGKPKVYIIQACRGEHRDPGEELRG 152
DB 141 LLSHGEEULIYKGD-GVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDGVQ--- 196
QY 153 NEELGDEBELGDEVAVLKNNPQ-SIPTYDTLHIYSTVEGLSTRHDEKSGFIQTLD 211
DB 197 -ADSGPINETDA-----NPRYKIPVEADFLFAYSTVPGYYSWRNPKGSGMFWQALCS 247
QY 212 VFIHKKGSILETEITRLMANTEVMOEGK-----PRKVNPEVOSTLRKKLY 258
DB 248 I-LDEHGKDLIMQILIRV--NDRVARHFESEQDDPCFNEKKQIPCMVSMLTKEYL 300

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